STIC-Biotech/ChemLib

31155

From:

Brunovskis, Peter

Sent:

Tuesday, December 12, 2000 6:45 PM

To:

STIC-Biotech/ChemLib

Subject:

sequence search on 09/051,034

Please search SEQ ID NOs:11, -12, and -13 of 09/051,034 against the commercial and interference databases using standard search parameters.

Please print results on laser printer and send to Peter Brunovskis, CM1-12E05. GAU 1632, 305-2471.

Thanks

Point of Contact:
Mona Smith
Technical Info. Specialist
CM1 12C14 Tel: 308-3278

Point of Contact:

Mona Smith
Technical Info. Specialist
CM1 12C14 Tel: 308-3278

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Scientific and Technical Information Center 3/155

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lease provide a detailed statement of the seasonalude the elected species or structures, key tility of the invention. Define any terms that mown. Please attach a copy of the cover she	words, synonyms, acrony it may have a special mea	ining. Give examples or i	. Wild Adding		
Fitle of Invention:			<u> </u>	•	
Inventors (please provide full names):				<u> </u>	
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

RESULT W49689

W49689 standard; Protein; 342 AA.

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WPI; 199
N-PSDB;
                                                                                                                                                                                                                                         Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose; sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig; graft tissue rejection; organ transplantation; xenotransplant.
Claim 4; Page 43-44; 71pp; French.
                  Transgenic non-human donors of organs for human containing DNA encoding antibodies that inhibit
                                                                                                                                                                                                                      Sus scrofa.
                                                                                                                                                                                                                                                                                      Porcine alpha-1,3-galactosyl transferase isoform
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                                                                                    Pourcel C,
                                                                                                         (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                19-JUL-1996;
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                                                    1998-112876/11.
DB; V49456.
                                                                                    Soulillou JP,
                                                                                                                                96FR-0009077.
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                                                                                     Vanhove B;
                     recipients -
graft rejection
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glycosyltransfer

*8888888888888

This sequence represents isoform 4 of the porcine enzyme appliants. 3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses are attachment of a galactose sugar molecule on the N-acetyllactosamine molecule on the N-acetyllactosamine molecules are partly responsible for raising anti-graft antibodies, which like to graft tissue rejection. The invention relates to a method of thin thin ting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing the diduction of the rejection response.

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This sequence represents isoform 3 of the porcine enzyme aligha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molecule are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants.
                                                                                                                                                                    Transgenic
containing
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 the galactose on
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DB; V49455.
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 the glycoproteins
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and glycolipids,
                                                                                                                                                                      recipients -
graft rejection
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R90573;
                                                                                                                                                                        The sequence is that of the product of the porcine Gal-alpha (1,3) galactosyl transferase gene which produces a Gal epitope on the surface of porcine cells. This epitope is recognised by antibodies which are responsible for hyperacute rejection of xenotransplanted pig cells, tissues and organs.
                  R90573 standard; Protein; 359 AA.
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                             WPI; 1994-317019/39.
N-PSDB; Q74712.
                                                                                                                                                                                                                                                                                                                                                                                                                                     {\sf Gal\mbox{-}alpha} (1,3) {\sf galactosyl} transferase; {\sf xenograft}; transplant; rejection.
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                                                                                                                                                                  See also
                                                                                                                                                                                                                              Disclosure; Page 35; 50pp; English.
                                                                                                                                                                                                                                                                                                        Mckenzie IFC,
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W49688

0 - NOV - 1998

(first entry)

igar; N-acet Maft tissue soform;

n; porcine; enzyme; alpha-1,3-galactosyl transferase; gal; N-acetyllactosamine; glycoprotein; glycolipid; antibody; tissue rejection; organ transplantation; xenotransplant.

pig;

Rorcine alpha-1,3-galactosyl transferase isoform 3.

भू4)9688 standard; Protein; 354 AA

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Local Similarity es 6; Conserv

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100.0%; Pr 100.0%; Pr

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15-JUN-1994;
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1 mnvkgr 6
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   levels of galactose he cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ب</u>
                                                                                                                                                                                                                                                               porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
ssue rejection; organ transplantation; xenotransplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mckenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page
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94US-0260201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rother RP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sandrin MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.8;
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RRESULT RESULT RES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the attachment of a galactose sugar molecule on the N-acetyllactosamine molecy found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic; swine; porcine; alpha (1,3) galactosyltransferase; antisense; ribozyme; Gal-alpha-1,3-Gal-beta-1-4GlcNAc; epitope terminal; xenogenic; transplant; rejection; gene therapy; pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                  (BIOT-) BIOTRANSPLANT INC.
(GEHO ) GEN HOSPITAL CORP.
(CHIL-) INST CHILD HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R85082 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                            WPI; 1995-373759/48
                                                                                 Baetscher MW, Gustafsson
                                                                                                                                                                                                                                                13-APR-1994;
                                                                                                                                                                                                                                                                                                      31-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                              WO9528412-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine alpha (1,3) galactosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 mnvkgr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents isoform 2 of the porcine a-1,3-galactosyl transferase (alpha-1,3-GT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Page 36-37; 71pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-human donors of organs for human recipients - {\tt DNA} encoding antibodies that inhibit graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 AA;
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Pred. No. 8.9
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                                                                                    Sachs DH;
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8.9;
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tiansferase corresplants
         New alpha-1,3-galactosyltransferase and leukaemia inhibitor factor georresp. DNA and nucleic acid constructs for inactivating the than significant for eliminating hyperacute region in human
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Sequence

Queny Match Best Local S Matches 6 (BRES-) (SVIN-) Alpha-1,3-galactosyltransferase; alpha-1,3-GalT; transgenic animal; pig; hyperacute rejection; xerotransplantation; donor organ; allograft rejection; Gal epitope; gene disruption; express AGT will not produce carbohydrate moieties contg. the distinctive terminal Gal-alpha-1,3-Gal-beta-1-4GlcNAc epitope, which is a significant factor in xenogenic (esp. human) transplant rejection of swine grafts. Therefore the swine cells produced in the AGT negative transgenic swine are xenogenic transplant rejection resistant, and can therefore be used by a transplant Crawford Sus scrofa. 26-JAN-1995; 27-JAN-1994; 03-AUG-1995. Pig alpha-1,3-galactosyltransferase. 11-DEC-1995 galactosyltransferase (AGT) R85082 is prevented, are prepd. by inhibiting the expression of the AGT gene T02892 using antisense gligonucleotides or ribozyme inactivators in a puripotent porcine embryonic stem cell. It is then inserted into a porcine occyte (from which the pronuclear material has been removed), which is itself grown to produce the transgenic swine. Swine which do not 27-JAN-1995; nomologous R76777; R76777 standard; Sequence gransgenic swine in which the normal claim 11; Pages 35-37; Novel transgenic alpha (1,3) galactosyl:transferase negative swine used to produce rejection resistant cells for xenogenic 1 MNVKGR 6 1 mnvkgr 6 1995-275446/36. DB; Q93077. BRESATEC LTD.
ST VINCENT'S HOSPITAL MELBOURNE LTD. Similarity 6; Conserv 8년, 371 or to provide gene therapy. Conservative (first Dapice 95US-0188607. 94US-0188607. 95WO-IB00088 Protein; 371 entry) AJF, 100.0%; 56pp; Pearse MJ, 0; English Score 31; DB Pred. No. 9.1; Mismatches expression of the alpha 16; 0; Length 371; Indels 0; Gaps 0;

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Matches 6
                           moiety found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, where the sugar transfer is the sugar rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                                                                                                             This sequence represents isoform 1 of the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine
                                                                                                                                                                                                                           Claim 4; Page 32-34; 71pp;
                                                                                                                                                                                                                                                       Transgenic non-human donors of organs for human recipients containing DNA encoding antibodies that inhibit graft rejec
                                                                                                                                                                                                                                                                                                                                               Pourcel C,
                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porcine alpha-1,3-galactosyl transferase isoform 1.
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                                                                                                                                                                                                                                                                                                                                                                            (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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1 mnvkgr
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DB; V49453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     porcine; enzyme; alpha-1,3-galactosyl transferase; gala-
-acetyllactosamine; glycoprotein; glycolipid; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AA;
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Pred. No.
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                                                                                                                                                                                                                                                       rejection
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Score 31; DB Pred. No. 9.2 0; Mismatches

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RESULT
Y26039
                                                                          The present sequence is a secreted protein nt746_4, encoded by known colone nt746_4 (deposited as ATCC 98600) isolated from human adult brain CDNA library. Recombinant secreted proteins can be produced by transforming host cells and culturing them under suitable conditions. The polynucleotide and protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Some predicted biological activities include cytokine and cell proliferation/ or suppressing activity, haematopoless regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, activity, catherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotide encoding secreted corrected protein can be used for gene therapy.
 Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein; cytokine; cell proliferation; immune stimulation; vaccine; immune suppression; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostasis; tirombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agostino MJ, Clark HF, Collins-Racie LA, Every Fechtel K, Jacobs K, Lavallie ER, McCoy JM, Steininger RJ, Treacy M, Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1998;
04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                             Claim 34; Page 115; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein nt746_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999
                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y26039 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                         1999-385352/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
   Similarity 83.
5; Conservative
                                                                            90
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97US-0067454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 100
                 90.3%;
Score 28; DB Pred. No. 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            human proteins
                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans
    0
                               Length 100
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    Indels
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07-NOV-1991

(first entry)

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RESULT 10
R80016
XX R80016
XX R80016
XX M80016
XX M80016
XX M80016
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XX M81pha-
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RESULT
R13750
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                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The amino acid sequence of the marmoset alpha-1,3-galactosyltransferase. The enzyme can be used in methods of enhancing an immune response by associating the alpha-galactosyl epitope with a cell membrane or viral glycoprotein. The alpha-galactosyl epitope enhances phagocytosis and subsequent processing of the antigen. The method is useful in the treatment of tumours e.g. leukemia, lymphoma, myeloma, melanoma, carcinoma and sarcoma, or for the generation of viral vaccines by opsonising a viral glycoprotein. The alpha-galactosyl epitope enhances recognition of the antigen in an animal that synthesises the naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-galactosyl epitope; cell membrane; virus; phagocytosis; tumour; antigen processing; leukemia; lymphoma; melanoma; carcinoma; sarcoma; vaccine; opsonisation; glycoprotein; antibody; anti-Gal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Association of an alpha-galactosyl epitope with a tumour or viral antigen - is administered to anti-Gal synthesising animals to ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Callithrix jacchus
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                                                            R13750;
                                                                                                                   R13750 standard; Protein; 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 9; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen - is admini
an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galili U,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R80016 standard; Protein; 376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         occuring antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1995;
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                                                                                                                                                                                                                                                            1 MNVKGR 6
||||:
1 mnvkgk 6
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DB; T04522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repik PM;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9405-0213200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-Gal.
                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 16;
Pred. No. 48;
                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 376;
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R45935

RAC R

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Best Local S
Matches 5
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14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intracellular or secreted proteins or lipids. These can be used for the prodn. of diagnostics and therapeutics. There is a single transmembrane domain consisting of a 19 amino acid hydrophobic segment flanked by basic residues and a large (presumably catalytic) C-terminal domain that would ultimately be targeted to the Golgi. It has potential N-glycosylation sites indicating that as with other glycosyltransferases, it may be synthesised as a glycoprotein. It is representative of a Type II transmembrane protein. See also R13749-R13752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The amino acid sequence codes for a protein capable of functioning as UDP- Gal: [beta-D-Gal(1.4)]-D-GlcNnc alpha (1.3)galacto-syltransferase. The products of this enzyme, sub-terminal alpha (1.3) and alpha(1.4) fucose residues are used in the post-
                                                                                    Gyycosyltransferase; fucosyltransferase; GDP-Fuc; in vitro; cell; surface; oligosaccharide.
                                                                                                                                                                         A glycosyltransferase
                                                                                                                                                                                                                                                                                            R45935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or polysaccharide or glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \begin{array}{l} \mathbb{G}\bar{\mathbb{p}}\text{P-Fuc:} \left[ \text{beta-D-Gal} (1,4/1,3) \right] \text{-D-GlcNAc} \left( / \mathbb{Glc} \right) \\ \mathbb{alpha} (1,3/1,4) \\ \mathbb{c} \text{ fucosyltransferase.} \end{array} 
                                                                                                                                                                                                                                      26-JUL-1994
                                                                                                                                                                                                                                                                                                                                                      R45935 standard; Protein; 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-1991;
                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowe JB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W@9112340-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |||||:
|36 mnvkgk 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eocal Similarity 83.
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNVKGR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1991-267151/36.
DB; Q13331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 AA;
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0627621.
90US-0479858.
90US-0480133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB Pred. No. 51; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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RESULT 13
W13639
ID W13639
XX W13639
XX W13639
XX U19-JUN
DE MUTINE
XX Alpha(
XX Alpha(
XX Alpha(
XX I3-MAR
XX I3-MAR
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XX UNNII
PR WPI: 1-DR W-PSDB
XX WPI: 1-DR W-PSDB
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PT cell s
XX Exampl
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Best Local Similarity
watches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a human glycosyl transferase. The emay be non glycosylated. This prevents premature loss of en activity. It can also be used in in vitro reactions to modi surface oligosaccharide mols. e.g. blood group determinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA fragment encoding a glycosyltransferase - can be used for in vitro reactions to modify cell surface oligosaccharide(s) e.g. blood gp. determinants, to protect against transplant rejection
            Example 2; Page 272-274; 329pp; English
                                  New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
                                                                                                                                                       08-SEP-1995;
                                                                                                                                                                             06-SEP-1996;
                                                                                                                                                                                                     13-MAR-1997
                                                                                                                                                                                                                            WO9709421-A1
                                                                                                                                                                                                                                                                         Alpha(1,3)-galactosyltransferase; glycosylation; oligosaccharide.
                                                                                                                                                                                                                                                                                                Murine alpha(1,3)-galactosyltransferase.
                                                                                                                                                                                                                                                                                                                        19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                       W13639 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                       Legault DJ,
                                                                                                                               (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also R45933-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 249pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                               36 mnvkgk 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNVKGR 6
                                                                                1997-192897/17
                                                                       T61676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                       Lowe JB;
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                       95US-0525058
                                                                                                                                                                               96WO-US13816
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                                                                                                                                                                                                                                                                                                                                                                       Protein; 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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oss of enzyme
to modify cell
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The present sequence represents a Staphylococcus aureus protein,
                                                             Claim 6;
                                                          Pages 321-322; 989pp; English
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can be used to

identify compounds

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e proteins of the interact with and

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Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reaction between UDP-Gal and N-acetyllactosamine and is associated with surface-localised expression of Gal(alpha1-3)Gal linkages. It amino acid sequence was deduced from a CDNA clone (T61676) obtd. by transfecting COS-1 cells with cDNA derived from mouse F9 teratocarcinoma cells, and screening the transfected cells for surface-localised Gal(alpha1-3)Gal linkages. When expressed in animal cell lines, the enzyme provides specific capabilities with respect to post-translational modification of the oligosaccharides of expressed proteins or lipids. The enzyme can also be used to raise antibodies and to screen for inhibitor cpds.
                                                                                                                                          Black MT,
Pratt JM,
                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcal gene; regulatory elevaccine; Staphylococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W27869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        galactosyltransferase (W13639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine UDP-Gal:beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)-
                                                 Novel polypeptide(s) from to isolate antimicrobial caureus infection
                                                                                                                                                                                                                                  19-FEB-1997;
                                                                                                                                                                                                                                                          21-AUG-1997
                                                                                                                                                                                                                                                                                    WO9730070-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W27869
                                                                                                                                                                                                         20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                         toxic shock syndrome.
                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||:
| 36 mnvkgk 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNVKGR 6
                                                                                                      1997-424969/39
DB; T83831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 83. 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of a hypothetical protein in AmyB 5' region (ORF1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394
                                                                                                                                          Burnham MK,
Reichard RW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                     /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus protein; ribozyme; antisense sequence; control;
gene; regulatory element; bacterial gene expression;
ylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ξ
                                                                                                                                                                                                                                                                                                                                                                                                                  aureus.
                                                                                                                                                                                                         96US-0011888
                                                                                                                                                                                                                                  97WO-US02318
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                          R₩,
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                                                                                                                                                                                                                                                                                                            "not specified"
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                                                                                                                                          Rosenberg M,
                                                                 n Staphylococcus aureus compounds, and in vacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                      encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB Pred. No. 51; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catalyses the a transglycosylation
                                                                                                                                          Knowles DJC, ward JM;
                                                                                                                                                                                                                                                                                                                                     GGN"
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                                                                 strain WCUH29
ines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 394;
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                                                                                                                                                         Nicholas
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RESULT 15
W38713
ID W38713
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Best Local S
Matches 4
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T cell immune
extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      based on homology with a Thermoanaerobacter thermosulfurogenes protein, is believed to be a hypothetical 35.6 kDa protein in AmyB 5' region (ORFI). The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic
           This sequence represents a Streptococcus pneumoniae protein that, based on homology with a B. lichenformis protein, is a glutamyl endopeptidase precursor, and is encoded by a DNA sequence of the invention. The DNA sequences were isolated from Streptococcus pneumoniae strain 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the
                                                                                                                                    diagnosing 
infections
                                                                                                                                                                                                                                             Black MT,
Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                       Claim 12;
                                                                                                                                                 Novel Streptococcus pneumoniae proteins and related DNA - useful diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                WPI; 1998-008793/01
N-PSDB; T98755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus

    pneumoniae glutamyl endopeptidase precursor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shock syndrome.
                                                                                                                                                                                                                                                                                                                                     14-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                WO9743303-A1
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nes 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 165 AA
                                                                                                                                                                                                                                                                                        SMITHKLINE BEECHAM PLC.
                                                                                                      Page 448; 483pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                          Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                   . 97WO-US07950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response; inoculation; antibody production; inhibitor response; antimicrobial compound; bacterial adhesion; matrix protein; protein-mediated cell invasion; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae
                                                                                                                                                                                                                                                                                                                                   96US-0017670
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66.7%;
                                                                                                                                                                                                                                                           Knowles DJC,
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Pred. No.
2; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic immunisation; antagonist;
                                                                                                                                                                                                                                                           Nicholas
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitor;
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88888888888888888 inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic infimunnisation. They can also be used to induce an immunological response the anamal by inoculation with the S. pneumoniae proteins or delivery and/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to bipock protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques. Sequence 165 AA;

밁 1 MNVKGR 6 |||:|| 13 mnvegr 18

Query Match 87.1 Best Local Similarity 83.3 Matches 5; Conservative 87.1%; 83.3%; Score 27; DB 19; Length 165; Pred. No. 34; 1; Mismatches 0; Indels

0;

Gaps

0;

Search completed: December 14, 2000, 10:11:09 Job 境價e: 43 sec

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Title:
Perfect score:
Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of
  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB seq length: 0
DB seq length: 2000000000
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/Packfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
 Query
Match Length
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Gapop 10.0 ,
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31
1 MNVKGR 6
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  GenCore version 4.5 (c) 1993 - 2000 Compugen
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         US-08-378-617A-10
US-08-249-613-6
US-08-249-613-6
US-08-378-617A-11
US-08-378-617A-12
US-08-378-617A-12
US-08-378-617A-12
US-08-525-058A-4
US-08-696-731-4
PCT-US91-00899-9
US-08-860-174A-12
US-08-860-174A-12
US-08-860-174A-12
US-08-860-174A-12
US-08-860-174A-12
US-08-860-174A-12
US-08-860-174A-12
US-08-902-233-3
US-08-551-171-3
US-08-551-171-2
US-08-902-233-7
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                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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3.695 Million cell updates/sec
Sequence 10, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 10, Appli
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Sequence 6, Appli
Sequence 8, Appli
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US-08-439-725A-14
US-08-441-629-12
US-08-867-471-14
US-08-867-471-19
US-08-138-439C-10
US-08-718-904-15
US-08-718-904-15
US-08-718-904-15
US-08-716-20712-12
US-08-551-171-5
US-08-551-171-6
US-08-551-171-6
US-08-464-1598-14
US-08-464-1598-14
US-08-951-822-27
ALIGNMENTS
                Sequence 14, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 14, Appl
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,617A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 06868/005001
FELECOMMUNICATION: NFORMATION:
TELEPHONE: (612) 335-5070
TELEPAX: (612) 38-9696
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CLARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-378-617A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: d'Apice, Martin J.

APPLICANT: Pearse, Martin J.

APPLICANT: Robins, Allan J.

APPLICANT: Robins, Allan J.

APPLICANT: Crawford, Robert J.

APPLICANT: Rathjen, Peter D.

TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
TITLE OF INVENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 120 South Sixth Street, Suite 2500

CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-08-378-617A-10
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Patent No. 5849991
                                                              Matches
                                                                                 Query Match
Best Local :
                                                            Local Similarity hes 6; Conserv
1 MNVKGR
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                                                            Conservative
                                                                                 100.0%;
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                                                                                 Score 31;
Pred. No.
                                                              Mismatches
                                                                                 DB 2;
                                                                                                  Length 371;
                                                              Indels
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1 MNVKGR 6

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US-08-886-863-6
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                                                                                                                                                                     Sequence 6, Application US/08886863 Patent No. 5824321
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                        GENERAL INFORMATION:
ARPLICANT: Haake, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 455-511
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Tumarkin Ph.D., Lisa A., REGISTATION NUMBER: P.8,347

REFERENCE/DOCKET NUMBER: PD-36

DELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                   STREET: 1880 Centur
CITY: Los Angeles
STATE: California
                                                                                    THILE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 10
GORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: IutA
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORRESPONDENCE ADDRESS
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pt no. 5643754
ERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              Local
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1880 Centu
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICANT: Haake, David A.
TLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN
MBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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         OUNTRY:
                                                                          DDRESSEE:
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                                                        E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
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1880 Century Park East, Suite 500
              USA
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                                                                                                                                                                                                                                                                                                                               score 28; DB Pred. No. 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 117;
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FLOW COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.,
REGISTATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: FD3602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Regents of the University of California TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/249, FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION: NAME: Tumarkin ph.D., Lisa A., REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PIMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                      FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                            STREET: 4225 Execu
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 5; Conserv
                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                              COUNTRY:
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/886,863
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1..117
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                                                                                                                       25-MAY-1995
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83.3%;
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Pred. No. 17;
1; Mismatches
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                                                                                                                                                                           Version #1.25
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17;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,617A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger; Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 06868/005001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 335-5070
Query Match
Best Local Similarity
5; Conserva
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                                                                                               ; MOLECULE TYPE: protein
US-08-378-617A-11
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US-08-378-617A-11
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                                                                                                                                     INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 584999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Crawford, Robert J.
APPLICANT: Rathjen, Peter D.
TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
TITLE OF INVENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 120 South Sixth Street, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 MNVRGR 30
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LOCATION: 1..117
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Robins, Allan J.
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                              90.3%;
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               Score 28; DB
Pred. No. 56;
1; Mismatches

    Mismatches

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                                                DB 2;
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                                                Length 368;
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RESULT 6
US-08-378-617A-12
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US-08-704-548-2
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Best Local Similarity 83...
Thes 5; Conservative
                                                                                                                                                                                                                     Sequence 2, Application US/08704548 Patent No. 5879675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,617A

FILING DATE: 26-JAN-1995

CLASSIFICATION: 435

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ellinger, Mark S.

REGISTRATION NUMBER: 34,812

REFERENCE/DOCKET NUMBER: 06868/005001

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 283-6566
                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: REPIX, PAIRICIA M.
APPLICANT: REPIX, PAIRICIA M.
APPLICANT: REPIX, PAIRICIA M.
APPLICANT: GOMPOSITIONS AND METHODS FOR VACCINES
TITLE OF INVENTION: COMPOSITIONS ALPHA-GALACTOSYL EPITOPES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (612) 288-9696
INFORMATION FOR SEO ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Fish & Richardson
STREET: 120 South Sixth Street, Suite 2500
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Crawford, Robert J.
APPLICANT: Rathjen, Peter D.
TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
TITLE OF INVENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. STREET: Suite 1800, Two Penn Center Plaza CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                       1 MNVKGK 6
                                                                                                                                                                                                                                                                                                                                                                                           1 MNVKGR 6
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Robins, Allan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 2;
Pred. No. 56;
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MEDIUM TYPE:

E: Floppy disk IBM PC compati

MPUTER READABLE FORM:

COUNTRY: US

USA

PA

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AUTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
NEGISTRATION UNMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPAX: (703)466-2347
                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
FILING DATE: 19920720
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                        GOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUTLE OF INVENTION: 1
THE OF INVENTION: 1
THE OF INVENTION: 1
THE OF INVENTION: 1
THE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                             STREET: 1755 Jef
CITY: Arlington
STATE: Virginia
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ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,548
FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EENGTH: 376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (215) 568-83
TELEFAX: (215) 568-5549
DRMATION FOR SEQ ID NO:
EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Monaco, Daniel A.
REGISTRATION UNMBER: 30,480
REFERENCE/DOCKET NUMBER: 87:
$LECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nce 4, Application US/07914281
t No. 5324663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNVKGK 6
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    P.C.
    1755 Jefferson Davis Highway, Fourth Floor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB Pred. No. 57; 1; Mismatches
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Query Match
Best Local Similarity
""+"hes 5; Conserv
                                                                                                    ; MOLECULE TYPE: protein US-08-393-246-4
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Patent No. 5595900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                        TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PATENTIN Releacement APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
APPLICATION NUMBER: US 07/914,281
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                               TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                       TYPE: amino acid TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1755 Je:
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                NAME: Lavalleye, Jean-Paul M. P. REGISTRATION NUMBER: 31,451 REFERENCE/DOCKET NUMBER: 2363-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 MNVKGK 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: P.C.
                                                                                                                                                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                        394 amino acids
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                                                                                                                                          unknown
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83.3%;
                                90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/393,246
                                  Score 28; DB
Pred. No. 60;
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                                                   Length 394;
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Conservative

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US-08-696-731-4
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NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPAX: (703)466-2347
TELEFAX: (703)466-2347
TELEFAX: (703)466-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      Sequence 4, Application US/08696731 Patent No. 5955347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08525058A Patent No. 5770420 GENERAL INFORMATION:
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLICOSACCHARIDE STREETUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF CLICOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURE
                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                            36 MNVKGK 41
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Local Similarity 83.3%;
les 5; Conservative
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 22202
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                                                                                                                                                                                                                          JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOHN B.
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Pred. No. 60;
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; MOLECULE TYPE:
US-08-696-731-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEFX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application PC/T GENERAL INFORMATION:
APPLICANT: Lowe, John B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC LOSS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/696,731
FILING DATE: 14-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/393,246
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method and Products For the Synthesis of TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids, TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned TITLE OF INVENTION: Genetic Sequences That Determine These Structur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-06
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 394 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/220,433 FILING DATE: 30-MAR-1994 APPLICATION NUMBER: US 07/914,281 FILING DATE: 20-JUL-1992
                                                                                                                                                                                                                 STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                         CITY: Arlington
                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 MNVKGK 41
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                                                                                                                                                                                                                                                                              1755 Jefferson Davis Highway, Suite 400
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                                                                                                                                                                                                                                                                                                                      SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                           Release #1.0, Version #1.25
                                                                   PCT/US91/00899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB Pred. No. 60; 1; Mismatches
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REGISTRATION NUMBER:

31,451

2363-021-55 PCT

RELEPHONE: (703)521-5940 REFERENCE/DOCKET NUMBER:

ELEFAX: (703)486-23

ELEPHONE:

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; TOPOLOGY: 1; MORECULE TYPE: US-08-860-174A-7
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Best Local Similarity
---*Ahes 5; Conserve
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                                                                                                                                         PROTOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILLING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New .....
STREET: 9th Floor, Eas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 MNVKGK 41
                                                                                                                                                                                                                                                                  RENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60-174A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATION FOR SEQ ID NO:
                                                                                                                            ENGTH:
                                                                                                                                                                                                                                      NPPLICATION NUMBER: US/08/860,174A
                                                                                                                                                                                                                                                                             EDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
DERATING SYSTEM: PC-DOS/MS-DOS DOS Text
OFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   OUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNVKGR 6
                                                                                                                                                                                                                                                                                                                        FUTER READABLE FORM:
EDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                  cal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ce 7, Application US/08860174A
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                                                                                                                               142 amino acids
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILSON, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERHOEIJEN, Martine Elisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAN DER LOGT, Cornelis Paul Erik
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                                                                                    protein
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83.9%; Suc.
100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A BIFUNCTIONAL OR BIVALENT ANTIBODY FRAGMENT ANALOGUE
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83.3%;
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; Pred. No. 60;
1; Mismatches
                   Score 26; pred. No.
       Mismatches
                   DB 2;
58;
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                             Length 142;
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       Indels
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       Gaps
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-860-174A-12
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US-08-860-174A-10
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                                                                                                                                                                                                           Sequence 10, Patent No. 5
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: August 14, 19
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
                                                                                   APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOELJEN, MARTLINE Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: AN TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                 NUMBER OF SEQUENCES:
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                 :: PILLSBURY, MADISON & SUTRO LLP 1100 New York Avenue, N.W.
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C;Species: Sus scrofa domestica C;Date: 21-Feb-1997 #sequence_re C;Accession: I46583 R;Strahan, K.M.; Gu, F.; Preece, Immunogenetics 41, 101-105, 1995 A;Title: cDNA sequence and chrom A;Reference number: I46583; MUID A;Accession: I46583	RESULT 1 145883 albha-1.3-galactosvitransferase		45 26 83	26 83	26 83	26 83	26 83	26 83	83	26 83	26 83	26 83	26 83	26 83	26 83	26 83	26 83	26 83	
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A;Experimental source: strain Bristol N2 C;Genetics:
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A; Molecule type: mRNA
A; Residues: 1-371 <STR>
                                                                                                                                                                                                     R;Gattung, S.; Pauley, A.
submitted to the EMBL Data Library, August 1999
A;Description: The sequence of C. elegans cosmid R04B3.
A;Reference number: Z20947
A;Accession: T30965
A;Map position: X
A;Introns: 42/1; 182/3; 222/2; 251/3; 322/1
A;Note: R0483.2
C;Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
                                                                                                                       A:Status: preliminary; translated A:Molecule type: DNA A:Residues; 1-378 < GAN' A:Cross-references: EMBL:U50198; F
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C;Superfamily: histo-blood
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A;Titje: Characterization of an alphal-->3-galactosyltransferase A;Reférience number: A39769; MUID:91201351
                                                                                                                                                                                                                                                                                                                                                                     N-acetyllactosaminide alpha-1,3-galactosyltransferase (EC 2.4.1.151) homolog C;Specides: Homo sapiens (man) C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 13-Sep-1998 C;Accession: A39769
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N;Alteshate names: hypothetical protein D1515

C;Specales: Saccharomyces cerevisiae

C;Dates: 15-reb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999

C;Accession: S61052; S67713
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C;Keywords: glycosyltransferase;
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A; Residues: 1-26 <JOZ>
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A; Reference number: S67708
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A; Residues: 1-454 < POW>
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A; Residues: 1-454 < POH>
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J. Biol. Chem. 267, 5534-5541, 1992
A;Title: Murine alpha-1,3-galactosvlt
A;Reference number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-368 <JO2>
A;Cross-references: GB:J04989; NID:g163123; PIDN:AAA30558.1; PID:g163124
C;Superfamily: histo-blood group 1 transferase
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
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                                                                                                                                                                 alpha-1,3-galactosyltransferase - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change C;Accession: I49698
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A;Accession: F70917
A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-371 <RES>
                                                           A; Reference number: A42117; A; Accession: I49698
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A;Title: Bovine alphal->3-galactosyltransferase:
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A; Residues: 1-308 <COL>
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alpha-1,3-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.145)
C;Species: Mus musculus (house mouse)
C;Decies: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 29-Sep-1999
C;Accession: A34417
R;Carsen, R.D.; Rajan, V.P.; Ruff, M.M.; Kukowska-Latallo, J.; Cummings, R.D.; Lowe, J.E Proc. Natl. Aced. Sci. U.S.A. 86, 8227-8231, 1989
A;Title: Isolation of a cDNA encoding a murine UDPgalactose:beta-D-galactosyl-1,4-N-acet A;Reference number: A34417; MUID:90046769
A;Accession: A34417; MUID:90046769
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-394 <LAR>
A;Cross references: GB:MJ6925; NID:9193419; PIDN:AAA37657.1; PID:g309242
C;Superfamily: histo-blood group 1 transferase; transmembrane protein
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A;Molecule type: mRNA
A;Residues: 1-376 <HEN>
A;Residues: 1-376 <HEN>
A;Cross-references: GB:S71333; NID:g558051; PIDN:AAB31587.1; PID:g558052
A;Cross-references: GB:S71333; NID:g558051; PIDN:AAB31587.1; PID:g558052
A;Note: authors translated the codon GTG for residue 251 as Ser
C;Superfamily: hlsto-blood group 1 transferase
C;Superfamily: hlsto-blood group 1 transferase; transmembrane prote:
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A;Title: Defining the minimal size of catalytically active A;Reference number: A56480; MUID:94331837
A;Accession: A56480
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C;Genetics:
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R.Krone, W.J.A.; Stegehuls, F.; Koningstein, G.; van Doorn, C.; Roosendaal, FEMS Microbiol. Lett. 26, 153-161, 1985
A.Fille: Characterization of the pColV-K30 encoded cloacin DF13/aerobactin o e sequence and primary structure.
A; Reference number: S01042
A; Reference number: S01042
A; Rocession: S01042
A; Arocession: S01042
A; Rocession: S0104
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A; Residues: 1-473 <KAW>
A; Cross-references: GB:AJ248286; GB:AL096836;
A; Cross-references: Strain Orsay
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R;Kawarabayasi, Y.; Sawada, M.;
M.; Ohfuku, Y.; Funahashi, T.;
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and g
A;Reference number: A71000; MUID
                                                                                                                                                                  probable ribose-phosphate pyrophosphokinase - Pyrococcus horikoshii C;Speckes: Pyrococcus horikoshii C;Deckes: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-C;Accession: C71207
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C71207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: Pyrococcus abyssi
A; Reference number: A75001
A; Accession: E75097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Genome: plasmid Colv-K30 C; Function:
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   and gene organization; MUID:98344137
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                                                                                                  Horikawa, H.; Haikawa, Y.; Hino, Y.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
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A; Access
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R;Smiths D.R.; Doucette-Stamm, L.A.; Deloughery, C; Lee, H; Dubois, J; Aldr
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; A;Tit Goldon, Complete genome sequence of the methanogenic archaeon, Methanococcus ja
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                                                                                                     A; Mole
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A; Residues: 1-322 <BUL>
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C; Supermanily: ribose-phosphate
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A; Note: this accession replaces an
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                                        Preferences: GB:AE000879;
Imental source: strain Dei
                                                                                                                                                                                                   D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, B.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan Ghurch, G.M.; Dankels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. Sriol. 179, 7135-7155, 1997
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Methanococcus jannaschii
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A:Molecule type: DNA
A:Residues: 20-21/T/,23-30,'L',32-88,'A',90-386 <LAN>
A:Residues: 20-21/T7,23-30,'L',32-88,'A',90-386 <LAN>
A:Cross-references: GB:J05516; GB:K02178; GB:M10426; GB:M1
R:Adams, M.D.; Wagner, L.M.; Graddis, T.J.; Landick, R.; A
J. Biol. Chem. 265, 11436-11443, 1990
A:Title: Nucleotide sequence and genetic characterization A;Reference number: A37074; MUID:90307651
A:Accession: A37074
                                                                     A;Note: this reported protein translation starts with R;Antonucci, T.K.; Landick, R.; Oxender, D.L. J. Cell. Biochem. 29, 209-216, 1987. Title: The leucine binding proteins of Escherichia c A;Reference number: 155524; MUID:86086153
A;Accession: 155524
                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-386 < PI
                                                                                                                                                                                                                                                                                                                            R; Plunkett, G. submitted to the EMBL Data A; Reference number: S47666 A; Accession: S47679
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 43-304,'AD',307-383,'AD',386 <OVC>
A;Experimental source: strain K12
A;Note: this protein was isolated from the per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The primary structure of a Leu, A;Reference number: A03415; MUID:77225636 A;Accession: A03415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 20-21,'T',23-30,'L',32-88,'A',90-386 <ADA>
A;Residues: 20-21,'T',23-30,'L',32-88,'A',90-386 <ADA>
A;Cross-references: GB:J05516; NID:9146630; PIDN:AAA83881.1; PID:9146631
R;Ovchinnikov, Y.A.; Aldanova, N.A.; Grinkevich, V.A.; Arzamazova, N.M.;
FEBS Lett. 78, 313-316, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: A23576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 260, 8257-8261, 1900
A;Title: The complete nucleotide sequences of the Escherichia
A;Reference number: A94677; MUID:85234531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Landick, R.; Oxender, D.L.
J. Biol. Chem. 260, 8257-820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 31-May-1979 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999 C;Accession: G65142; A23576; A37074; A03415; S47679; I55524 R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y.
A; Molecule type: DNA
A; Residues: 20-21, 'T'
                                                                                                                                                                                                    A;Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18435.1; PID:g912457 A;Note: this reported protein translation starts with a GTG codon; it has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000422; GB:U00096; NID:g1789868; A;Experimental source: strain K-12, substrain MG1655
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A; Residues: 1-386 <BLAT>
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C;Superfamily: conserved
                                                  A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names:
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83.3%;
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,23-30,'L',32-88,'A'

,90-386

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A.CCOSS-references: GB:M29377; NID:g146628; FIDN:AAA24075.1; PID:g146629
A.GGANE: LAVJ
A.HMAP DOSALLON:
C.FRUNCLION:
A.CESS-FIDIO: Specifically binds Leu, 11e, and Val and may be involved in their transme produced capture to the company of the component of the
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GATR PIG
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Y78J_RORU
Y76J_CAEEL
Y08J_RORU
Y76J_RORU
Y78J_RORU
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12.117 Million cell updates/sec
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 p41480 autographa
03410 tactococcus
006372 orgyia pseu
058195 methanococc
p11102 influenza b
p13884 influenza b
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p36433 influenza b
p046436 agrobacteri
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044346 agrobacteri
p52179 homo sapien
p10767 homo sapien
p10768 mus musculu
060319 methanococc
p80894 antechinus
p01236 homo sapien
p55151 macaca mula
p48802 brachydanio
p15728 rhizobium 1
p54604 bacillus su
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2 escherichia
3 methanococc
6 caenorhabdi
6 human cytom
5 influenza b
1 caenorhabdi
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0 rhodospiril
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ALIGNMENTS

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RESULT ASSOCIATED ASSO
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SEQUENCE
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Q21697;
Q1-00Y-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 39, Last annotation update)
POTATIVE N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
(EC 3.5.1.26) (GLYCOSYLASPARAGINASE) (ASPARTYLGLUCOSAMINIDASE) (NECTYL-BETA-GLUCOSAMINYL)-L-ASPARAGINE AMIDASE) (AGA).
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HSSP; P20933; 1APZ.
WORMPEP; R04B3.2; CE07412
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Rhabditidae; Peloderinae; Caer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100 6; Conservative
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POTENTIAL.
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Caenorhabditis.
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                   GLYCOSYLASPARAGINASE, A
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GLYCOSYLASPARAGINASE, E
SIMILARITY
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

SPEGSLFWIYQSK -> R (IN SHORT ISOFORM).

M -> I (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFC715E8D89993D4 CRC64;
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(POTENTIAL).
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I sequences in human genomic DNA.";

I sequences in human genomic DNA.";

I J. BLO1. Chem. 264:14290-14297(1989).

- i- FUNCTION: TRANSFER OF GALACTOSE FROM UDP-GALACTOSE TO AN CEPTOR MOLECULE (R).

- i- CATALYTIC ACTIVITY: UDP-GALACTOSE + BETA-D-GALACTOSYL-1,4-

N-ACETYL-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.

C BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.

C - i- COFACTOR: MANGANESE.

- i- COFACTOR: MANGANESE.

- i- COFACTOR: MANGANESE.

- i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUNG FORM IN TRANS CISTERNAE OF GOLGI.
                      Query Match
Best Local
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Best Local
                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
N-ACETYLLACTOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE (EC 2.4.1.151)
(GALACTOSYLTRANSFERASE) (UDP-GALACTOSE:BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLICOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 89340543.
JOZIASSE D.H., Sha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Boyine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                          Signal-anchor;
                                                                                                                                                                                                                                                                   PIR; A44785;
Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shaper N.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTA1
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01-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNVKGR 6
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Similarity
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                                                                                                                                                                                                                                  A44785.
Glycosyltransferase; Glycoprotein;
ir; Golgi stack; Manganese.
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                                                                                                                                                                                                                                                                                                             AAA30558.1;
                                                                                                                     ΑA;
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                                                                                                           1 stack;
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                      90.3%;
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                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOOD GROUP AB ?
SIMILARITY WITH
Score 28; DB
Pred. No. 15;
1; Mismatches
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                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31;
Pred. No.
                                                                                                                     SBC50D6737BDDC33 CRC64;
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                                               Length 368
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                                                                                                                                                                                                                                                                Transmembrane
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                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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А.J
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Query Match
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GATR_MOUSE
                                                                                          CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *MUTIAL ALPHA 1.3 - GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.

*PAULIANSE D.H., Shaper N.L., Kim D., van den Eijnden D.H., Shaper J.H.;

*MUTIAL Alpha 1.3 - galactosyltransferase. A single gene locus specifies four isoforms of the enzyme by alternative splicing.";

*J. Biol. Chem. 267:5534-5541(1992).

-I- FUNCTION: TRANSFER OF GALACTOSE FROM UDP-GALACTOSE TO AN ACCEPTOR MOLECULE (R).

-I- CATALYTIC ACTIVITY: UDP-GALACTOSE + BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
N-ACETYLLACTOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE (EC 2.4.1.151)
(GALACTOSYLTRANSFERASE) (UDP-GALACTOSE:BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                   Transferase: Glycosyltransferase: Glycoprotein: Transmembrane:
Signal-anchor: Golgi stack: Alternative splicing: Manganese.
DOMAIN
1 41 CYTOPLASMIC (POTENTIAL).
TRANSMEM 42 60 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                            EMBL; M26925; AAA37657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UDPgalactose:beta-D-galactosyl-1,4-N-acetyl-D-glucosaminide alpha-1,3-galactosyltransferase: expression cloning by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P23336;
                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 92184813.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Larsen
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                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: MANGANESE.

COFACTOR: MANGANESE.

COFACTOR: MANGANESE.

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.

SIMILARITY: STRONG, TO BLOOD GROUP AB TRANSFERASE.

SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOSYLTRANSFERASES.
                                                                                                                                                                                                               A34417; A34417.
MGI:95704; GGTA1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.D., Rajan V.P.,
                                                                            42
61
83
319
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FERRIC AEROBACTIN R
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SEQUENCE
                                                                                                                                                    Receptor.
SIGNAL
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                                                                                                                                        CHAIN
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Bacteria; Proteobacteria;
                                                                                                                                                                          Outer membrane;
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    -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
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HYPOTHETICAL PROTEIN MJ0371
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                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
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P90838;
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Science 273:1058-1073(1996).
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                                Unpublished observations
                                                                Filipowicz W.;
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INTERPRO; IPR001233; -
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PROSITE; PS01288; UPF0027; 1.
Hypothetical protein.
SEQUENCE 505 AA; 55230 MW; D528F
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                                                                                                                                                                                                                                    Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.("Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";

Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                            EMBL; X17403; CAA35356.1;
EMBL; M15120; AAA45997.1;
PIR; B26793; WMBES1.
PIR; S09846; S09846.
                                                                                                                                                                                                                                                                                           MEDLINE; 90269039.
Chee M.S., Bankier
Horsnell T., Hutch
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 87112940.
Rueger B., Klages S., Walla
Tomlinson P., Barrell B.G.;
                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                    virion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses;
                                                                                                                                                                                                                                                                                                                                                                     "Primary structure and transcription virion phosphoproteins pp65 and pp71 J. Virol. 61:446-453(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Betaherpesvirinae; Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 MNVEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNVKGR 6
                                                                                                                                                                                                                      r. Top. Microbiol. Immunol. 154:1 SIMILARITY: BELONGS TO THE UL82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytomegalovirus (strain
es; dsDNA viruses, no RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 06, Created)
(Rel. 11, Last sequence update)
(Rel. 37, Last annotation update)
MATRIX PHOSPHOPROTEIN (PP71).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                              В.,
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Pred.
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                                                                                                                                                                                                                        154:125-169(1990).
UL82 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D528F702E2586909 CRC64;
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No.
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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                    cytomegalovirus.";
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Phosphorylation;

Matrix protein. A; 61948 MW; F

F2F73FE652654659 CRC64;

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RESULT
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Best Local S
Matches 5
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Best Local Similarity
Matches 4; Conserv
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13-AUG-1987 (Rel. 05, I
01-MAY-1992 (Rel. 22, I
NUCLEOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long. Its content use by non-profit institutions as long as its content use by non-profit institutions as long. Usage by an obtained and this statement is not removed. Usage by an obtained the statement is not removed.
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Briedis D.J., Tobin M.;
"Influenza B virus genome: complete nucleotide sequence of influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 6 encoding the influenza B/lee/40 virus genome RNA segment 6 encoding the influenza B/lee/40 virus genome RNA segment 6 encoding the influenza B/lee/40 virus genome RNA segment 6 encoding the influenza B/lee/40 virus genome RNA segment 6 encoding the influenza B/lee/40 virus genome RNA segment 6 encoding the influenza B/lee/40 virus genome RNA segment 6 encoding the influenza B/lee/40 virus genome 8 encoding the influenza B/lee/40 virus geno
                                                                                                                                                                                                                                                                                              UN52_CAEEL STANDARD; PRT; 2481 AA (006561; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAEEL
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P04665;
SEQUENCE FROM N.A. MEDLINE; 93339574. Rogalski T.M., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                         BASEMENT MEMBRANE
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                                                                                                                                      Rhabditidae; Peloderinae;
                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                          UNC-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00506; flu_virus_nuc;
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nes 5; Conserv
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ssRNA negative-strand viruses; Orthomyxoviridae;
a virus A and B group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133:448-455(1984)
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                                                                                                                                                                                                                                                                         PROTEOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61770 MW;
                                                                                                                                                                            Nematoda;
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83.3%;
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Last sequence up
Last annotation
      B.D.,
                                                                                                                                      Caenorhabditis
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Pred. No.
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Pred. No. 40;
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          Mullen G.P.,
                                                                                                                                                                        Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74C4FEAF9E75A695 CRC64;
                                                                                                                                                                                                                                                                     PRECURSOR (PERLECAN HOMOLOG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
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40;
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          Moerman D.
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                 INTERPRO; IPRO03006
PFAM; PF00047; 19;
PFAM; PF00052; lami
PFAM; PF00053; lami
PFAM; PF00057; ld1_
PFAM; PF00057; ld1_
PFAM; PF00051E; PS001186; E
PROSITE; PS01186; E
PROSITE; PS0119; I
PROSITE; PS01209; I
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HSSP; P01130;
INTERPRO; IPRO
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONE VERY SHORT FORM AND TWO LONG FORMS.

-I- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANE OF ALL CONTRACTILE TISSUES. IT IS CONCENTRATED OVER MUSCLE DENSE BO AND M-LINES WHICH ARE ASSOCIATED WITH BETA-INTEGRIN.

-I- DEVELOPMENTAL STAGE: SYNTHESIZED EARLY IN EMBRYOGENESIS.
-I- SIMILARITY: CONTAINS 3 LDL-RECEPTOR CLASS A DOMAINS.
-I- SIMILARITY: CONTAINS 16 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-I- SIMILARITY: CONTAINS 7 LAMININ EGF-LIKE DOMAINS.
-I- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
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SIGNAL
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INTERPRO;
INTERPRO;
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Genes Dev. 7:1471-148
-!- FUNCTION: PROBABI
                                                                        DOMAIN
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SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

ALTERNATIVE PRODUCTS: UNC-52 PRODUCES AT LEAST THREE POLYPEPTIDES:
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068; LDLRA_2; 3.
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
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IN EGF-LIKE 3 (INCOMPLETE).

IN EGF-LIKE 4 (N-TERMINAL).

IN DOMAIN IV 2.

IN EGF-LIKE 5.

IN EGF-LIKE 5.

IN EGF-LIKE 7.

IN EGF-LIKE 7.

IN EGF-LIKE 6.

IN EGF-LIKE 7.

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STRAIN-168 / JH642;
MEDLINE; 95219086;
Takemaru K.-I., Mizuno M., Sato T.,
Takemaru K.-I., Mizuno M., Sato T.,
"Gömplete nucleotide sequence of a s
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IG-LIKE C2-TYPE DOMAIN 13.
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IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 16.
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Pred. No. 1.9e+02;
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      T., Takeuchi M., Kobayashi
a skin elément excised by
in Bacillus subtilis.";
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EMBL; D84432; BAA12410.1; -
EMBL; Z99117; CAB14545.1; -
SUBTILIST; BG11285; YQBN.
Hypothetical protein.
SEQUENCE 149 AA; 17137 M
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      EMBL; X55387; CAA39062.1;
PIR; S12260; S12260.
Hypothetical protein.
NON_TER 184 184
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Bacteria; Proteobacter
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Medigue C.,
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5; Conserv
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C., Moszer I.,
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                                                                                                                                                                                                                                                                                                    Majewski C., Trebst A.;
"The pet genes of Rhodospirillum rubrum: cloning the genes for the cytochrome bol-complex.";
Mol. Gen. Genet. 224:373-382(1990).
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Virology 202:586-605(1994).
-1- SIMILARITY: TO THE CORRESPONDING PROTEIN OF OPMNPV.
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MEDLINE; 97271300.
Ahrens C.H., Russell F
Rohrmann G.F.;
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3_NPVOP
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"Molecular characterization of the restriction endonuclease (scrFIR) associated with the ScrFI restriction/modification from Lactococcus lactis subsp. cremoris UC503.";
Microbiology 143:2277-2286(1997).
-!- CATALYTIC ACTIVITY: RECOGNIZES THE DOUBLE-STRANDED SEQUE AND CLEAVES AFTER C-2.
                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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EMBL; D13768; BAA02911.1; EMBL; U75930; AAC59092.1;
                                                                                                                                                                                              polyhedrosis virus genome.
Virology 229:381-399(1997)
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Russell R.L.Q., Rohrmann G.
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HYPOTHETICAL 54.9 KDA PROTEIN.
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                                                                                                                                            331 LNVKGR
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L; S71333; AAB31587.1;
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SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
                                                                                                                                                                                                                        Similarity
5; Conserv
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V->*: NO CHANGE IN ACTIVITY.
; 13C490C0BF2FA2DF CRC64;
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MISSING: NO ACTIVITY.
I->*: 100% DECREASE IN ACTIVITY.
MISSING: 79% DECREASE IN ACTIVITY.
MISSING: 70% DECREASE IN ACTIVITY.
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(TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
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EMBL; AB022664; BAA85629.1; -.

INTERPRO; IPR002100; -.

INTERPRO; IPR002487; -.

PFAM; PF00319; SRF-TF; 1.

PFAM; PF01486; K-box; 1.

PRNITS; PR00404; MADSDOMAIN.

PROSITE; PS50066; MADS_BOX_2; 1.

SEQUENCE 218 AA; 24908 MW;
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01-AUG-1998
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287AA LONG H
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Mitochondrion.
Eukaryota; Viridiplantae; Embry
Magnoliophyta; eudicotyledons;
Magnoliophyta; erabidopsis.
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01-JUN-2000
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Eukaryota; Viridipl
Gnetophyta; Gnetops
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155 VNVKGR 160
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SEQUENCE 107
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les 5; Conservative
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Genet. 0:0-0(0).
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dons; Rosidae; eurosids II;
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AX Yamamoto S., Sekine M., Baba S.-I., KOSUgi H., HoSOyama A., Nage
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ogux
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RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RASUChi Y., Shizuwa H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hype
"Thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
"Cha Res. 5:55-76(1998).

LOA Res. 5:
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                                                                                                                                                                                                                                                                                                                               Mar. Environ. Res. 0:0-0(2000).
EMBL; AF19250; AAF15278.1; .
INTERPRO; IPRO00014; .
INTERPRO; IPRO01092; .
INTERPRO; IPRO03015; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Rarchner S.I., Kennedy S.W., Trudeau S., Hahn M.E.;
"Towards a molecular understanding of species differences in
sensitivity; initial characterization of Ah receptor cDNAs in
and an amphibian.";
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Archaea; Euryarchaeota;
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Eukaryota; Metazoa; 'Amphibia; Batrachia;
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                                                                                                                                                                                                                                                                                                                                               Chen Y. -H., Ho K.-C.;
"Wiccleotide sequence of tuf gene of a phytoplasma associated Logifah witches' broom.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF086617; AAD48153.1; -.
                                                                                                                                                                                                                                            INTERPRO; IPRO00795; -.
PFAM; PF00009; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNFCT
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
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                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
               Wilson R., Ainscough
Bonfield J., Burton
                                                                    SEQUENCE FROM N.A. MEDLINE: 94150718.
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M04G12.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 420 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reducing archaeon Archaeoglobus Nature 390:364-370(1997).
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01-JAN-1998 (TIEMBLTel. 05, Las
01-JAUC-1998 (TIEMBLTel. 07, Las
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=VC-16 / DSM 4304 / MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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83.3%;
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               Connell M., Copsey T., Cooper
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1.7e+02;
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Best Local S
Matches 5
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Best Local S
Matches 5
                                   O18261
O18261;
O18261;
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-UN-2000 (TrEMBLrel. 14,
UNC-52 PROTEIN.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematod
Rhabditidae; Peloderinae; C
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OSGIO:
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TREMBLrel. 1
T13015.1 PROTEIN.
T13015.1.
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EMBL; 281103; CAB03210.1; -
HSSP; P16068; LAWN.
INTERPRO; IPRO01054; -
SEQUENCE 686 AA; 78588 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T33015 genomic sequence.";
"Arabidopsis thaliana chromosome III BAC T3015 genomic sequence.";
"Bublidopsis thaliana chromosome III BAC T3015 genomic sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; T
Magnoliophyta; eudroctyledons; Rosidae;
Brassicaceae; Arabidopsis.
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                                         oda; Chromadorea; Rhabditida; Rhabditoidea;
Caenorhabditis.
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1; Mismatches
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2.8e+02;
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Brassicales;
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PFAM; PF00047; ig; 2.
PFAM; PF00053; LBMININ_EGF; 5.
PFAM; PF00053; LBMININ_EGF; 3.
PFO0051TE; PS00202; EGF_1; UNKNOWN_4.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 7.
PROSITE; PS01248; LAMININ_TYPE_EGF; 7.
PROSITE; PS01248; LAMININ_TYPE_EGF; 7.
PROSITE; PS003031; -; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9XTD2 PRELIMINARY;
Q9XTD2;
Q9XTD2;
Q1-NOV-1999 (TrEMBLrel. 12, C
Q1-NOV-1999 (TrEMBLrel. 12, L
Q1-JUN-2000 (TrEMBLrel. 14, L
UNC-52 PROTEIN.
UNC-52 OR ZC101.2.
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HSSP; P01130; 1LDR.
WORMPEP; ZC101.2B; CE15030.
INTERPRO; IPR000034; -.
INTERPRO; IPR000551; -.
INTERPRO; IPR002049; -.
INTERPRO; IPR002172; -.
INTERPRO; IPR003006; -.
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-!- ALTERNATIVE PRODUCTS: FOUR FORMS; ISOFORM ZC101.2A
ISOFORM ZC101.2B (SHOWN HERE), ISOFORM ZC101.2C (Q9
ISOFORM ZC101.2E (Q9XTI5); MAY BE PRODUCED BY ALTER
                         INTERPRO; IPRO(INTERPRO; IPRO)
PFAM; PF00047;
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                                                                                               INTERPRO;
INTERPRO;
INTERPRO;
INTERPRO;
                                                                                                                                                                                             SPLICING.

EMBL; Z93395; CAB07707.1; -.

EMBL; Z93375; CAB07707.1; JOINED.

EMBL; Z93375; CAB07568.1; -.

EMBL; Z93395; CAB07568.1; JOINED.

WORMPEP; ZC101.2C; CE15034.
                                                                                                                                                                                                                                                                                                                                              Percy C., Baynes C.;
submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-:- ALTERNATIVE PRODUCTS: FOUR FORMS; ISOFORM ZC101.2A (
-:- ISOFORM ZC101.2B (018261), ISOFORM ZC101.2C (SHOWN H
ISOFORM ZC101.2E (09XTI5); MAY BE PRODUCED BY ALTERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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5; Conserv
                                                                   IPR003006;
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  laminin_B;
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83.3%;
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1; Mismatches
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REAM: PF00057; ldl_recept_a; 3.

REAM: PF00057; ldl_recept_a; 3.

REAM: PF00051; LDLRECEPTOR.

REAM: PF00021; EGF_1; UNKNOWN_4.

REAM: PF000215; MITOCH_CARRIER; UNKNOWN_1.

REAM: PF000215; PS00248; LDLRA_1; 3.

REAM: PF000215; PS00248; LDLRA_1; 3.

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347 INVKGR 352
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H. pylori cytoplas
Porcine alpha-1,3-
Porcine alpha-1,3-
Galactosyl transfe
Pig alpha(1,3)-gal
Porcine alpha-1,3-
Porcine alpha (1,3)
                                                                                                  Secreted protein n
Marmoset alpha-1,3
GDP-Fuc:[beta-D-Ga
A glycosyltransfer
                                                                                                                                                                     Description
                                                                                          Murine alpha(1,3)-
    WPI; 1999-385352/32.
N-PSDB; X80674.
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04-DEC-1997;
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ALIGNMENTS

Agostino MJ, Clark HF, Fechtel K, Jacobs K, La Steininger RJ, Treacy M, Secreted protein; cytokine; cell proliferation; immune stimulation; vaccine; immune suppression; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostasis; thrombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour; gene therapy. (GEMY) GENETICS INST INC. Clark HF, Corrand Jacobs K, Lavallie ER, Wong GG; 98US-0203106. 97US-0067454. 98WO-US25512 Collins-Racie LA, МсСоу , MC Evans Merberg Ç D

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RESULT RE
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conditions and conditions in humans and cell proliferation/
conditions include cytokine and cell proliferation/
conditions activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activiny, inhibin activity, chemotactic/chemokinetic activity, activity, activity, cadherin/tumour invasion suppressor activity, and the tumour inhibition activity. The polynucleotide encoding secreted
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                                                                                                                                      Disclosure; Fig 9; 85pp; English
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                                                                                                                                                                                                                                       Association of an alpha-galactosyl epantigen - is administered to anti-Gal
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N-PSDB; T04522.
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Pred. No. 4.5;
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The amino acid sequence of the marmoset alpha-1,3-galactosyltransferase. The enzyme can be used in methods of enhancing an immune response by respectating the alpha-galactosyl epitope with a cell membrane or viral

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         The amino acid sequence codes for a protein capable of functioning sa a UDP- Gal:[beta-D-Gal(1.4)]-D-GlCNAC alpha (1.3)galacto-syltransferase. The products of this enzyme, sub-terminal alpha (1.3) and alpha(1.4) fucose residues are used in the post-translational modification of the oligosaccharides on cell-surface, intracellular or secreted proteins or lipids. These can be used for the prodn. of diagnostics and therapeutics. There is a single transmembrane domain consisting of a 19 amino acid hydrophobic segment flanked by basic residues and a large (presumably catalytic) C-terminal domain that would ultimately be targeted to the lumen of the Golgi. It has two potential N-glycosylation sites indicating that as with other glycosyltransferases, it may be synthesised as a glycoprotein. It is representative of a Type II transmembrane protein. See also R13749-R13752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                      12-DEC-1990;
14-FEB-1990;
14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein. The alpha-galactosyl epitope enhances phagocytosis and subsequent processing of the antigen. The method is useful in the treatment of tumours e.g. leukemia, lymphoma, myeloma, melanoma, carcinoma and sarcoma, or for the generation of viral vaccines by opsonising a viral glycoprotein. The alpha-galactosyl epitope enhances recognition of the antigen in an animal that synthesises the naturally
                                                                                                                                                                                                                                                                     e.g. the present polysaccharide
                                                                                                                                                                                                                                                                                                                                                                              Lowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \label{eq:gdp-Fuc:beta-D-Gal(1,4/1,3)]-D-GlcNAc(/Glc)alpha(1,3/1,4)-fucosyltransferase.}
                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                    Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or polysaccharide or glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                WPI; 1991-267151/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R13750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R13750 standard; Protein; 394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 occuring antibody - anti-Gal.
                                                                                                                                                                                                                                                                                                                                                                                                       (UNMI ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 AA;
                                                                                                                                                                                                                                         Fig 2; 155pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          OF MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0479858.
90US-0480133.
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Pred. No.
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                                                                                                                                    ll-surface,
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RESULT
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Best Local
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                                                                                                                                                                     The sequence is that of a human glycosyl transferase. The enzyme may be non glycosylated. This prevents premature loss of enzyme activity. It can also be used in in vitro reactions to modify ce surface oilgosaccharide mols. e.g. blood group determinants. See also R45933-9.
 19-JUN-1997
                  W13639;
                                  W13639 standard; Protein; 394 AA.
                                                                                                                                                      Sequence
                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                       DNA fragment encoding a glycosyltransferase - can be used vitro reactions to modify cell surface oligosaccharide(s) blood gp. determinants, to protect against transplant reje
                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                    WPI; 1994-048874/06
                                                                                                                                                                                                                                                                                                                                      20-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                         surface; oligosaccharide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A glycosyltransferase
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                                                                                                            Local Similarity
nes 6; Conserv
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                                                                                            1 MNVKGK 6
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6; Conserv
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                                                                                                                                                       394 AA;
                                                                                                           100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                        Fig 2; 249pp; English.
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 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 394 AA.
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Pred. No.
                                                                                                                     Score 31;
Pred. No.
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                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   vitro; cell;
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W20717
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Best Local S
Matches 6
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N-PSDB; T61676.
                                                          Vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnos cytoplasmic; genome replication; transcription; recombination
                                                                                                      H. pylori cytoplasmic protein,
                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                       15-JUL-1997
                                                                                                                                        W20717;
                                                                                                                                                       W20717 standard; protein; 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Example 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine alpha(1,3)-galactosyltransferase
                    WO9640893-A1
                                   Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Legault DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                   Local Similarity hes 6; Conserv
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                                                                                                                                                                                                          1 MNVKGK 6
                                                                                                                                                                        σ
                                                                                                                                                                                                mnvkgk 41
                                                                                                                                                                                                                                                                              394 AA;
                                                                                                                                                                                                                                   Conservative
                                                                                                                       (first entry)
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05cp20518orf56

ritis; diagnosis; recombination;

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Murine UDP-Gal:beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)-galactosyltransferase (W1639) catalyses the a transglycosylation reaction between UDP-Gal and N-acetyllactosamine and is associated with surface-localised expression of Gal(alphal-3)Gal linkages. Its amino acid sequence was deduced from a cDNA clone (T61676) obtd. by transfecting COS-1 cells with cDNA derived from mouse F9 teratocarcinoma cells, and screening the transfected cells for surface-localised Gal(alphal-3)Gal linkages. When expressed in animal cell lines, the enzyme provides specific capabilities with respect to post-translational modification of the oligosaccharides of expressed proteins or lipids. The enzyme can also be used to raise antibodies and to screen for inhibitor cpds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell surface oligosaccharide structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant fucosyltransferase proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha(1,3)-galactosyltransferase; glycosylation; oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 272-274; 329pp; English.
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                            100.0%;
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Score 31; DE
Pred. No. 19;
0; Mismatches
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19;
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RESULT
W4960
XX W496
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DT 10 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC typylori infection or to identify H. pylori polypeptide binding CC compounds, useful as potential H. pylori polypeptide activators or CC inhibitors. The genomic sequence of H. pylori (ATCC 55679) was CC determined from overlapping contigs generated by mechanically CC shearing the bacterial DNA. The sequences were analysed for ORF of CC determined the nucleotides, and the predicted coding regions defined CC decimal contiguences were analysed for ORF of CC vaccine development, the amino acid sequences predicted from CC vaccine development, the amino acid sequences predicted from CC vaccine development, the amino acid sequences predicted from CC vaccine development, the amino acid sequences predicted from CC vaccine development, and the production determined CC the sequences of interest, particular regions can be isolated from CC H. pylori by PCR amplification for recombinant polypeptide CC vaccines of interest, particular regions can be isolated from CC H. pylori by PCR amplification for recombinant polypeptide
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Matches 5; Conser
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Best bocal :
                                                                                                                                                                                                                                                                                                                                   sugar; N-acetyllactosamine; grafft tissue reference;
                                                                                                                                                                                                                       FR2751346-A1.
                                                                                                                                                                                                                                                                                Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W49689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                          19 JUL-1996;
                                                                                                                                                                    23-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                 Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pörcine alpha-1,3-galactosyl transferase isoform 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    involved in genome replication, transcription, repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a Helicobacter pylori cytoplasmic protein involved in genome replication, transcription, recombination and
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N-[PSDB; T67970.
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                         rejection; organ transplantation; xenotransplant.
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                                                                                                           96FR-0009077.
                                                  96FR-0009077
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95US-0487032.
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Pred. No. 48;
1; Mismatches
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Best Local S
Matches 5
             Claim 4; Page 39-41; 71pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents isoform 4 of the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molety found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1.3-GT into the cells of animal,
                                    Transgenic non-human donors of organs for human recipients containing DNA encoding antibodies that inhibit graft rejection % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                    Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
graft tissue rejection; organ transplantation; xenotransplant.
                                                                                                                                                                                                                                                                                                                                                                                                               W49688;
                                                                             WPI; 1998-112876/11
N-PSDB; V49455.
                                                                                                                                                                                                                                                                             Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                                                                  Pourcel C,
                                                                                                                                           (INRM ) INSERM
                                                                                                                                                                        19-JUL-1996;
                                                                                                                                                                                                  19-JUL-1996;
                                                                                                                                                                                                                            23-JAN-1998
                                                                                                                                                                                                                                                   FR2751346-A1
                                                                                                                                                                                                                                                                                                                                                         Porcine alpha-1,3-galactosyl transferase isoform
                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                       W49688
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DB; V49456.
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-human donors of organs for human recipients - {\tt DNA} encoding antibodies that inhibit graft rejection
                                                                                                                    Soulillou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                              INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                    Vanhove B;
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Pred.
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No.
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77;
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RESULT
R62508
                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents isoform 3 of the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molecty found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The results relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gal-alpha (1,3) galactosyl transferase; xenograft; transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galactosyl transferase clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R62508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                             The sequence is that of the product of the porgalactosyl transferase gene which produces a surface of porcine cells. This epitope is recomminded to the product of which are responsible for hyperacute rejection
                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R62508 standard;
                                                                                                               galactosyl transferase gene which pro
surface of porcine cells. This epito
which are responsible for hyperacute
pig cells, tissues and organs.
                                                                                                                                                                                                                                                                                          WPI; 1994-317019/39.
                                                                                                                                                                                                                                                                                                                      Mckenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                               16-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09421799-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rejection.
                                                                       Sequence
                                                                                                                                                                                                     Disclosure; Page 35; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
mes 5; Conserv
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                                                                                                                                                                                                                              sequences encoding Gal-alpha (1,3)galactosyl transferase clones contg. such sequences are used in xenograft therapies
                                                                                                    also
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                                                                                                                                                                                                                                                                                                                      Sandrin MS
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              90.3%;
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Pred. No.
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                DB
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Bd
                               15;
                                                                                                                              porcine Gal-alpha (1,3)
a Gal epitope on the
recognised by antibodies
tion of xenotransplanted
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                               Length 359
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RESULT 11
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ID W49687
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AC W49687
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DT 10-NOV
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DE Porcin
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R90573
ID R9
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                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                 Matches
                                                                                                                                                                                                                             Pig alpha(1,3)-galactosyltransferase (R90573) was expressed in monkey COS cells following transfection of the cells with vector pGT which contains an insert including the encoding CDNA (T12242). Co-transfection of these cells with vector pHT encoding human H-transferase (R90572) resulted in a reduction in the levels of galactose alpha(1,3) galactose epitopes expressed
                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-049326/05
N-PSDB; T12242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-1996
                                       W49687;
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                Redn. of rejection of xenogeneic cells following transplantation by introducing a vector expressing fucosyl:transferase into the
                                                                                                                                                                                                                                                                                                                                                                                             Fodor WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1994;
15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha(1,3)galactosyltransferase; xenograft hyperacute rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pig alpha(1,3)-galactosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R90573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R90573
                   10-NOV-1998
                                                          W49687 standard;
                                                                                                                                                                                                                      by the cells.
                                                                                                                                                                                                                                                                                                   Example 2; Page 52-54;
                                                                                                                                                                                                                                                                                                                                                                                                               (ALEX-) ALEXION PHARM INC (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9534202-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplantation; galactose alpha(1,3) galactose
                                                                                                         1 MNVKGK 6
||||:
1 mnvkgr 6
                                                                                                                                                Local Similarity
nes 5; Conserv
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                                                                                                                                                  Conservative
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                   (first entry)
                                                                                                                                                                                                   AA;
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94US-0260201
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                                                          Protein; 363
                                                                                                                                                            90.3%;
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Pred.
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80
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                                                                                                                                                                    Length 359;
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Porcine alpha-1,3-galactosyl transferase isoform

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RESULT 12
R85082
     PFF PF N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Bocal Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents isoform 2 of the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GI). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molecule from the necessary of the surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, which the did to graft tissue rejection. The invention relates to a method of impubiling the graft rejection mechanism by introducing the sequence engoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants. Newtralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
31-MAR-1995;
                                                                                                                  Thansgenic; swine; porcine; alpha (1,3) galactosyltransferase; antisense; ribozyme; Gal-alpha-1,3-Gal-beta-1-4GlcNAc; epitope terminal; xenogenic; transplant; rejection; gene therapy; pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic non-human donors of organs for human recipients - containing DNA encoding antibodies that inhibit graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose; sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig; guart tissue rejection; organ transplantation; xenotransplant.
                                26 - OCT - 1995.
                                                           WO9528412-A1
                                                                                                                                                                             Poscine alpha (1,3) galactosyltransferase
                                                                                                                                                                                                           04-JUN-1996
                                                                                                                                                                                                                                                                R85082 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPA; 1998-112876/11.
N-PSDB; V49454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pourcel C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-1996;
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     95WO-US03940
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                                                                                                                                                                                                                                                                                                                                                                                                             90.3%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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RESULT
R76777
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           galactosyltransferase (AGT) R85082 is prevented, are prepd. by inhibiting the expression of the AGT gene T02892 using antisense oligonucleotides or ribozyme inactivators in a pluripotent porcine embryonic stem cell. It is then inserted into a porcine occyte (from which the pronuclear material has been removed), which is itself grown to produce the transgenic swine. Swine which do not express AGT will not produce carbohydrate moieties conty, the distinctive terminal Gal-alpha-1,3-Gal-beta-1-4GlcNAc epitope, which is a significant factor in xenogenic (sep. human) transplant rejection of swine grafts. Therefore the swine cells produced in the AGT negative transgenic swine are xenogenic transplant rejection resistant, and can therefore be used by a transplant
                                                                                                                                                                                 pig; hyperacute rejection; xerotransplantation; donor organ;
allograft rejection; Gal epitope; gene disruption;
homologous recombination; knock-out.
                                     26-JAN-1995;
27-JAN-1994;
                                                                            27-JAN-1995;
                                                                                                      03-AUG-1995
                                                                                                                               WO9520661-A1
                                                                                                                                                         Sus scrofa.
                                                                                                                                                                                                                     Alpha-1,3-galactosyltransferase; alpha-1,3-GalT; transgenic animal;
                                                                                                                                                                                                                                                Pig alpha-1,3-galactosyltransferase
                                                                                                                                                                                                                                                                         11-DEC-1995
                                                                                                                                                                                                                                                                                                                          R76777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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(GEHO)
(CHIL-)
(SVIN-) ST VINCENT'S HOSPITAL MELBOURNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic swine in which the normal expression of the alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baetscher MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recipient,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel transgenic alpha (1,3) galactosyl:transferase negative swine used to produce rejection resistant cells for xenogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-APR-1994;
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||||:
1 mnvkgr 6
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                                                                                                                                                                                                                                                                                                                        standard; Protein; 371
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GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or to provide gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding porcine alpha-1,3-GalT was generated from liver RNA using primers based on conserved regions of the mouse and cattle alpha-1,3-GalT genes. Potential sites to interrupt the alpha-1,3-GalT gene (via homologous recombination) were identified in exons 4, 7, 8 and 9. Such inactivation allows the breeding of 'knock-out' animals, e.g. pigs suitable as donors of organs to overcome hyperacute rejection
This sequence represents isoform 1 of the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine
                                                                                                                                                                                                                                                                                                                                                                                                                   Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
graft tissue rejection; organ transplantation; xenotransplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-275446/36.
N-PSDB; Q93077.
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N-PSDB; V49453.
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                                                                                                             Transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porcine alpha-1,3-galactosyl transferase isoform
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                                                                                           non-human donors of organs for human recipients - DNA encoding antibodies that inhibit graft rejection
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                                                                                            The present sequence represents a Salmonella typhimurium peptide sequence. The Salmonella nucleotide (X83935), its complement (X83936) and fragments (X83937 to X83971), are useful for detecting and diagnosing Salmonella infection in humans, animals and food. The nucleotides will detect many, if not all Salmonella species especially Salmonella dublin, S. enteritidis, S. gallinarum, S. minnesota, S. paratyphi (types A, B and C), S. pullorum, S. typh ty21a and S. typhimurium. The fragments may be used to construct a DNA chip, useful for the simple and inexpensive testing of substances for the presence of Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecty found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, wh lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                                                                                                                                                                                                                                                            WPI; 1999-418268/35
N-PSDB; X83964.
                                                                                                                                                                                                                                                     Disclosure; Column 187-190;
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US-08-378-617A-12
US-08-704-548-2
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3.695 Million cell updates/sec
   Sequence
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Sequence
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9, Appli
9, Appli
1, Appli
1, Appli
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2, Appl
4, Appl
4, Appl
4, Appl
4, Appl
4, Appl
10, Appl
10, Appl
11, Appl
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	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25
	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6	80.6
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AT TOWNERS	US-09-023-082A-140	US-09-023-082A-132	US-09-023-082A-128	US-09-023-082A-124	US-09-023-082A-120	US-09-023-082A-112	US-09-023-082A-96	US-09-023-082A-136 .	US-09-023-082A-70	US-09-023-082A-80	PCT-US95-06764-6	US-09-023-082A-72	US-08-886-863-6	US-08-249-013-6	US-09-023-082A-74	US-09-023-082A-82	US-09-023-082A-76
	Sequence 140, App	Sequence 132, App	Sequence 128, App	Sequence 124, App	Sequence 120, Ap	Sequence 112, App	Sequence 96, App.	Sequence 136, App	Sequence 70, App.	Sequence 80, App.	Sequence 6, Appl:	Sequence 72, App.	Sequence 6, Appl:	Sequence 6, Appl:	-	Sequence 82, Appi	-
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ALIGNMENTS

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; MOLECULE TYPE: protein US-08-378-617A-11
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US-08-378-617A-11
                                                                                                                                                 TELEFAX: (612) 288-9696
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: d'Aplee, Anthony J.F.
APPLICANT: Pearse, Martin J.
APPLICANT: Robins, Allan J.
APPLICANT: Robins, Allan J.
APPLICANT: Robins, Allan J.
APPLICANT: Rathjen, Peter D.
TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
TITLE OF INVENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 120 South Sixth Street, Suite 2500
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,617A
FILING DATE: 26-AN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 06868/00500:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: POS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
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Local Similarity les 6; Conserv
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    Conservative
                         100.0%;
    0;
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  Score 31; DB
Pred. No. 20;
0; Mismatches
                                               Length 368;
      0
      Gaps
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RESULT 3
US-08-704-548-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 371 amin
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local (
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                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: GALILI
APPLICANT: REPIK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 0686
TEMECOMMUNICATION INFORMATION:
TELEPHONE: (612) 335-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Crawford, Robert J.
APPLICANT: Rathjen, Peter D.
TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
TITLE OF INVENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR VACCINES TITLE OF INVENTION: COMPRISING ALPHA-GALACTOSYL EPITOPES NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT: Pearse, l
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                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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COUNTRY > USA
                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson STREET: 120 South Sixth Street, Suite 2500
                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 1 MNVKGK 6
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                                     Philadelphia
                  PA
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                                                    E: SEIDEL, GONDA, LAVORGNA & MONACO, P.C Suite 1800, Two Penn Center Plaza
                                                                                                                                                             GALILI, URI
REPIK, PATRICIA M.
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anthony J.F
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US-07-914-281-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (215) 568-5549 INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/704
FILING DATE: 11-SEP-1996
CLASSIFICATION: 424
ATTORNEX/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF CLICOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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LENGTH: 376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                   TELEPHONE: (703)521-45
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
                                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1755 Jefferson Davis Highway, Fourth Floor
                                      (703)521-4500
(703)486-2347
                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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Pred. No. 21;
0; Mismatches
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TOPOLOGY: unknown ; MOLECULE TYPE: protein US-07-914-281-4
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Best Local Similarity
Matches 6; Conserv
                                                                   Query Match 100.0%; Score 31; Best Local Similarity 100.0%; Pred. No. Matches 6; Conservative 0; Mismatch
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                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION UMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAVALLEY, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPHONE: (703)521-4500
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

LOWE, JOHN B.
                                                                                                                                                                                                                                       TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF CLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: A
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                                                                                                                                                                                                        TOPOLOGY:
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36 MNVKGK 41
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                                  MNVKGK 6
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GY: unknown
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Pred. No. 21;
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APPLICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAVALIEY, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)486-2347
TELEFAX: (703)486-2347
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-525-058A-4
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                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-696-731-4
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                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08696731 Patent No. 5955347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                   36 MNVKGK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 6; Conserv
                                                                                   ADDRESSEE: OBLC
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                        Arlington
Virginia
Y: U.S.A.
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1755 Jefferson Davis Highway, Fourth Floor
                                                            1755 Jefferson Davis Highway, Fourth Floor
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                                                                                                     OBLON,
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                                                                                                                                                                    METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 100.0%; Pred. No. 21;
                                                                                                       SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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OMPUTER: IBM PC compatible PERATING SYSTEM: PC-DOS/MS-DOS OUTER READABLE FORM:
EDIUM TYPE: Floppy disk

Version #1

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Matches 6; Conserv
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENGTH: 394 amino acids
                                                                                                                                                                    EMPP: 2202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-Paul
NAME: 31,451
                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/696,731
EXILING DATE: 14-AUG-1996
GLASSIFICATION: 435
PROOF APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                 STATE: VII
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/393,246
RETLING DATE:
APPLICATION NUMBER: US 08/220,433
RILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
RETLING DATE: 20-JUL-1992
                                                                                                                                                                                                                                                                                                STREET: 1755 Jen
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-00899-9
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                                                                                                                                                                                                                                                                                                                                                                DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                    RESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     DIE OF INVENTION: Method and Products For the Synthesis of DIE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids, DIE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned DIE OF INVENTION: Genetic Sequences That Determine These Structur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6-731-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ce 9, Application PC/TUS9100899
AL INFORMATION:
LICANT: Lowe, John B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNVKGK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AME: Lavalleye, Jean-Paul M. P.
EGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                       ER OF SEQUENCES:
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                                                                                                                                                                                                                                                                               Virginia
                                                                                                                                                                                                                                                                                                                       1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                            OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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  2363-021-55 PCT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703)521-5940
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
                                                                                                         APPLICATION NUMBER: US/08/378
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 335-5070
                                                                              TELEFAX: (612) 288-9696
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: YES ORIGINAL SOURCE: TISSUE TYPE: Blood
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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MOLECULE TYPE: pro
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                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity tes 6; Conserv
               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                ZIP: 55402
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          : 371 amino acids
amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                               120 South Sixth Street, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rathjen, Peter D.
WENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
WENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; nilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robins, Allan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d'Apice, Anthony J.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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Query Match Best Local Similarity

90.3%;

Score Pred.

28; No. DB 87;

Length 371;

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US-08-946-329A-76

; Sequence 76, Application US/08946329A

; Patent No. 6057091
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Patent No. 5925522
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Beachy, Philip A.
APPLICANT: POITCE, Jeffrey H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
FILING DATE: Unknown
FILING DATE: Unknown
                                                                                                                         TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 3.50°, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                    417 MNVRGK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Washington Way
CITY: Richland
STATE: Washington
                                                                   STREET: 4225 E:
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: none
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                                                                                                           ADDRESSEE:
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                                                                                      E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 amino acids
                                    USA
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Intellectual Property Services
Battelle Memorial Institute
PNNL P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.K.; Saffer, J.D. N: A Salmonella Sequence, Methods Of Detection N: Of A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella Sequence, And Methods Of Detection Of Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 2;
Pred. No. 1.1e+02;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/061,323
FILING DATE: 07-0CT-1996
APPLICATION NUMBER: 08/729,743
FILING DATE: 10-70L-1996
APPLICATION NUMBER: 08/567,357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349,498
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/1
                 APPLICATION NUMBER: US/08/441,629
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,217
FILING DATE: 22-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patticia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kirschner, Marc W
APPLICANT: Kinoshita, No. 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
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                                                                                                                                                                                                                                                                                                                           STREET: Two Militia I CITY: Lexington STATE: Massachusetts
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COMPUTER: IE
   REFERENCE/DOCKET NUMBER: HU95-01A
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Pred. No. 43;
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; MOLECULE TYPE:

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Matches 5; Conserv
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TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERICANT: Kirschner, Marc W.

PERICANT: Kinoshita, No. 60807181yuki
PERICANT: Kinoshita, No. 60807181yuki
PERICANT: Kinoshita, No. 60807181yuki
PERICANT: Receptor-Ligand Assay
PERICANTON NUMBER: US/08/776,207A
UNREANT APPLICATION NUMBER: US/08/776,207A
PERICATION NUMBER: PCT/US95/09172
PARAMER APPLICATION NUMBER: US/07-19
PARAMER FILING DATE: 1995-07-19
PARAMER FILING DATE: 1995-05-15
PARAMER APPLICATION NUMBER: 08/279,217
PARAMER APPLICATION NUMBER: 08/279
PARAMER APPLICATION NUMBER: 08/279
PARAMER APPLICATION NUMBER: 
COMPUTER, READABLE FORM:
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LENGTH: 187 amino acids
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GANISM: Xenopus laevis
776-207-11
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                                                                                                                                                                                                                       PLICANT: Kirschner, Marc W.
PLICANT: Kinoshita, Noriyuki
TEC OF INVENTION: RECEPTOR-LIGAND ASSAY
MARC OF SEQUENCES: 17
RESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNVKGK 6
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les 5; Conserv
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WARE: FastSEQ for Windows Version 3.0
D NO 11
CTH: 187
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STRANDEDNESS: sir
                                                                                                        CITY: Lexington
STATE: Massachusetts
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                           nce 11, Application PC/TUS9509172 RAL INFORMATION:
                                                                                                                                                                   NDDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.STREET: Two Militia Drive
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No. 6080718
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83.3%;
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Pred. No.
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73;
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Search completed: December 14, 2000, 10:11:40 Job time: 74 sec

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-307-896-4
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                                                   Query Match
Best Local Similarity
The Symptomic Conserve
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Best Local Similarity
Watches 5; Conserv?
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                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILE REFERENCE: 29770
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08307896C Patent No. 6034071
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/307,896C CURRENT FILING DATE: 1994-09-16 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/279,217
FILING DATE: 22-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,629
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
ANAME: CESSIVE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: HU95-01A PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240

TELEPAY. (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
401 INVKGK 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/09172
                                  1 MNVKGK 6
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                                                                       Conservative
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Pred. No. 1.6e+02;
1; Mismatches (
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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   length: 2000000000
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Match
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ALIGNMENTS

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RESULT A39769

N-acetyllactosamine 3-alpha-galactosyltransferase (EC 2.4.1.124) - bovine C;Species: Bos prinigenius taurus (cattle) C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 29-Sep-1999 C;Accession: A44785 C;Accession: A44785 D.H.; Shaper, J.H.; Van den Eijnden, D.H.; Van Tunen, A.J.; Shaper, N.L. J. Biol. Chem. 264, 14290-14297, 1989 A;Title: Bovine alphal-3-galactosyltransferase: isolation and characterization of a A;Reference number: A44785; MUID:89340543 A;Accession: A44785 A4785; MUID:89340543 A;Accession: A44785 A4785 A;Status: not compared with conceptual translation A;Residues: 1-368 CJOZ> R;Joziasse, D.H.; Shaper, J.H.; Jabs, E.W.; Shaper, N.L.
J. Blol. Chem. 266, 6991-6998, 1991
A;Title: Characterization of an alphal-->3-galactosyltransferase homologue on human
A;Reference number: A39769; MUID:91201351
A;Accession: A39769
A;Status: preliminary N-acetyllactosaminide alpha-1,3-galactosyltransferase (EC 2.4.1.151) homolog C;Species: Homo sapiens (man) C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 13-Sep-1998 RESULT A44785 Š A;Molecule type: DNA A;Residues: 1-26 <JOZ> C:Superfamily: histo-blood group 1 transferase C;Keywords: glycosyltransferase; hexosyltransferase C; Accession: A39769 A;Cross-references: GB:J04989; NID:g163123; PIDN:AAA30558.1; PID:g163124 C;Superfamily: histo-blood group 1 transferase C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein 밁 Query Match Best Local S Matches 6 Query Match Best Local Matches Local Similarity hes 6; Conserv Local Similarity nes 6; Conserv 1 MNVKGK 6 1 MNVKGK 6 N Conservative Conservative 100.0%; 100.0%; 0 0 Score 31; DB Pred. No. 1.2; Score 31; Pred. No. Mismatches Mismatches DB 2; Length 26; DB 2; Length 368; 0 Indels Indels 0 0 Gaps Gaps

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A;Refegence number: A34417;
A;Accession: A34417
A;Status; preliminary
                                                                                                                     alpha-1/3-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC C;Speckes: Mus musculus (house mouse)
C;Datek-115-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 29-Sep-1999
C;Accession: A34417
R;Larsen, R.D.; Rajan, V.P.; Ruff, M.M.; Kukowska-Latallo, J.; Cummings, R.D.
Rroc. Wattl. Acad. Sci. U.S.A. 86, 8227-8231, 1989
A;Title: Isolation of a cDNA encoding a murine UDPgalactose:beta-D-galactosylands-companylation of a cDNA encoding a murine uDPgalactose:beta-D-galactose:beta-D-gala
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A;Resignes: 1-376 <HEN>
A;Resignes: 1-376 <HEN>
A;Crossifreferences: GB:S7133; NID:g558051; PIDN:AAB31587.1; PID:g558052
A;Noteb authors translated the codon GTG for residue 251 as Ser
C;Supergamily: histo-blood group 1 transferase
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane prote
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A;Title Defining the minimal size of catalytically active A;Reference number: A56480; MUID:94331837
A;Accession: A56480
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C;Specwes: Callithrix sp.
C;Date: [19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
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A;Accession: I49698
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Specties: Mus musculus (house mouse)
C;Datte: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
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A; Residues: 1-371 < RE
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A;Titles Murine alpha-1,3-galactosyltransferase: A single
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R; Joziasse, D.H.
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7, 5534-5541, 1992
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                                                              A; Residues: 1-386 <PLUV

A; Cross references: EMBL:U00039; NID:9466582; PIDN:AAB18435.1; PID

A; Note: this reported protein translation starts with a GTG codon;

R; Antonucci, T.K.; Landick, R.; Oxender, D.L.

J. Cell. Biochem. 29, 209-216, 1985

A; Title: The leucine binding proteins of Escherichia coli as model:

A; Reference number: 155524; MUID:86086153
                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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A;Molecule type: DNA
A;Residues: 20-21,'T',23-30,'L',32-88,'A',90-386 <ADA>
A;Residues: 20-21,'T',23-30,'L',32-88,'A',90-386 <ADA>
A;Cross references: GB:J05516; NID:g146630; PIDN:AAA83881.1; PID:g146631
R;Ovchinnikov, Y.A.; Aldanova, N.A.; Grinkevich, V.A.; Arzamazova, N.M.;
FEBS Lett. 78, 313-316, 1977
FEBS Lett. 78, 313-316, 1977
A;Title: The primary structure of a Leu, Ile and Val (LIV)-binding proteina; Reference number: A03415; MUID:77225636
A;Accession: A03415
A; Reference number: S47666
                                                                                                                                                        A; Molecule type: protein
A; Residues: 43-304, 'AD', 307-383, 'AD', 386 < OVC>
A; Experimental source: strain K12
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A;Residues: 20-21,'T',23-30,'L',32-88,'A',90-386 <LAN>
A;Residues: 20-21,'T',23-30,'L',32-88,'A',90-386 <LAN>
A;Cross-references: GB:J05516; GB:K02178; GB:M10426; GB:M10427;
A;Cross-references: GB:J05516; GB:K02178; GB:M10426; GB:M10427;
A;Common Common Common
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J. Biol. Chem. 260, 8257-8261, 1985
A;Title: The complete nucleotide sequences
A;Reference number: A94677; MUID:85234531
A;Accession: A23576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M26925; NID:g193419; PIDN:AAA37657.1; PID:g309242 C;Superfamily: histo-blood group 1 transferase C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane prote:
                                                                          A; Note: this protein was R; Plunkett, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G65142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000422; GB:U00096; NID:g1789868; PIDN:AAC76485.1; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A37074
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sion: G65142; A23576; A37074; A03415; S47679; I55524
er, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNVKGK 6
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3ibson, A.L
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A;Gene: livy
A;Map position: 76 min
C;Function:
A;Description: specifically binds Leu, Ile, and Val and may )
C;Superfamily: LIV-binding protein
C;Superfamily: (or 20-42) signal sequence #status predicted
F;1-42/Domain: (or 20-42) signal sequence #status predicted
F;43-386/Product: leucine/isoleucine/valine-binding protein
F;95-120/Disulfide bonds: #status experimental
              S14619 B
S14619 branched-chain amino acid-binding protein livJ -
N; Alternate names: LIV-binding protein livJ
C; Species: Citrobacter freundii
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C; Accession: S14619
R; Dagget Garvin, L.; Hardies, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Fel
C;Accession: F71804; A71826
R;Alm, RA:, Ling, L.S.L.; Moir, D.T.; King,
; Ives, C.; Gibson, R.; Merberg, D.; Mills,
Nature 397, 176-180, 1999
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Best Local Similarity
Thes 5; Conserve
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C:Superfamily: ompR protein; response regulator homology
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A;Residues: 1-213 <AR2>
A;Cross-references: GB:AE001551; GB:AE001439; NID:g4155887;
A;Experimental source: strain J99
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A; Experimental source: strain J99
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A; Residues: 1-213 <ARN>
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C; Species: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                             ;Keywords: phosphoprotein
;5-115/Domain: response regulator homology <RRH>
;53/Binding site: phosphate (Asp) (covalent) #status predicted
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:Residues: 20-21,'T',23-30,'L',32-88,'A',90-386 <RES>
:Cross-references: GB:M29377; NID:gl46628; PIDN:AAA24075.l; PID:gl46629
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137 LNVKGK
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Pred. No. 41;
1; Mismatches
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Pred. No.
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April 1991
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Taylor, D.E.;
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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y. M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Y. DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the A;Reference number: A71000; MUID:98344137
A;Accession: A71025
A;Status: preliminary; nucleic acid sequence not shown; A;Status: preliminary; nucleic acid sequence
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A; Status: preliminary
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A; Residues: 1-367 < DAG>
A: Cross-references: EMBL: X58820;
C: Superfamily: LIV-binding protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: PH1494
C; Superfamily:
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A; Residues: 1-369 <KAW>
A; Residues: 1-369 <KAW>
A; Cross-references: GB: AP000006; NID: g3236133; PIDN: BAA30601.1; PID: g3257918
A; Experimental source: strain OT3
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                                                                                                                                                                                                                alpha-1,3-galactosyltransferase - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
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                                                                  A; Molecule type: mRNA
A; Residues: 1-371 <ST
                                                                                                                  A; Reference number: A; Accession: I46583
                                                                                                                                   A; Title: cDNA sequence and chromosome localization A; Reference number: I46583; MUID: 95104914
                                                                                                                                                                                   R; Strahan, K.M.; Gu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note:
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                                                                                                     A;Status:
                                                                                                                                                                    Immunogenetics 41, 101-105,
                                                 A;Cross-references:
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Best Local
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                  GGTA1
                                                                                               preliminary; translated from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 83. 5; Conservative
   histo-blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus
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                                                                  <STR>
                                                   GB:L36152;
                                                                                                                                                                    F.; Preece,
01-105, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.3%;
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protein
group 1
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                                                   NID: g642635; PIDN: AAA73558.1;
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                                                                                                                                                                                     A.F.; Gustavsson,
                                                                                                                                                                                                                                                                                                                                                                                                        ::
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Pred. No.
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Yamazaki,
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J.; Kushida,
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Query Match Best Local

Similarity

83

Score Pred.

28; No.

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2

Length

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υ. μιου. Chem. 256, 10293-10305, 1981
A;Titue. Primary structure of 3-phosphoglycerate mplete isequence of the enzyme.
A;Reference number: A92292; MUID:8201117777
A;Accession: A92292
A;Molecule turn
                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoglycerate Kindse (50 2.....) phosphoglycerate Kindse (50 2....) phosphoglycerate Kindse (50 2....) phosphoglycerate Capacitic horse) c.specifies: Equus caballus (domestic horse) c.patier 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Feb-1997 c.accession: A92292; A00669
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A; Status:
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Best Local Similarity
Frances 5; Conserve
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R;Gatting, S.; Pauley, A.

submitted to the EMBL Data Library, August 1999

cosmid R04B3
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A;Experumental source: strain Bristol N2
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A; Residues: 1-378 <GAT>
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Introns: 42/1; 182/3; 222/2; 251/3; 322/1
Note: R04B3.2
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                                                  Best
                                                               Query Match
                                                                                                            eyords: acetylated amino end; ATP; gluconeogenesis; glycolysis; AMOS field site: acetylated amino end (Ser) #status experimental 1950/3/Binding site: ATP (Lys, Glu) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 MNVKGR 332
                                                                                                                                                                                           Sequence, structure and activity of phosphoglycerate kinase: a possible hinge-
phose number: A93209; MUID:79199779
ephts: annotation; X-ray crystallography, 2.5 angstroms; muscle
pent: The structure consists of two discrete, globular domains that are joined by
the form a helix associated with the amino-terminal domain.
                                                                                                                                                                                                                                                                                                                         dues: 1-416 <MER>
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                                                                                                                                                              family: phosphoglycerate kinase
                                                Local
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 1 MNVKGK 6
                                                                                                                                                                                                                                                                                          R.D.; Blake, C.C.F.; Evans, P.R.; Haser, R.; Rice, D.W.; Hardy, G.W.; Merrett, 79, 773-777, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; translated from GB/EMBL/DDBJ
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                               Similarity
5; Conserv
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                               Conservative
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Pred.
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Mismatches
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339
A;Accession: C72591
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                                                                                                                                                                                              A;Cross-references: EMBL:AF060869;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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A; Residues: 1-463 <WON>
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A; Accession: T14884
                                                                                                                                                                                                                                                                                                                        A; Title: Identification and ovar typhimurium LT2.
                                                                                                                                                                                                                                                                                                                                                           R; Wong, K.K.; McClelland, M.; Stillwell, L.C.; Sisk, E.C.; Thurston, S.J.; Saffer, Infect. Immun. 66, 3365-3371, 1998
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A;Residues: 1-458 <KAW>
A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80185.1;
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C;Accession: C72591
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Best Local S
Matches 5
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Best Local Similarity
Matches 5; Conser
417 MNVRGK 422
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                                                                     Similarity 83. 5; Conservative
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83.3%;
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                                                                       Score 28; DB Pred. No. 84; 1; Mismatches
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Pred.
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synGAP-b1 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T13958

submitted to the EMBL Data A; Description: SynGAP-bl.

Library,

August 1998

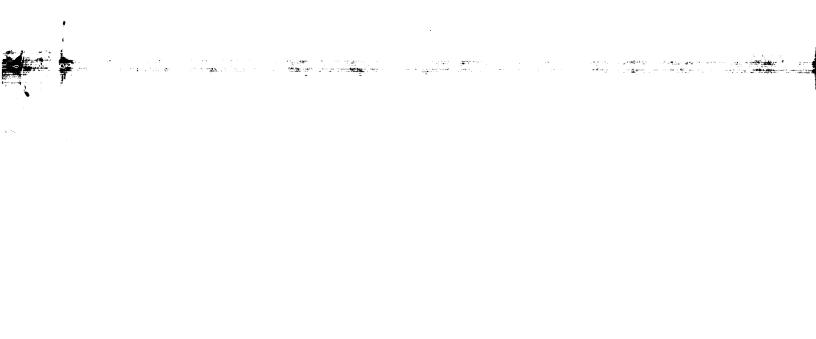
R; Suzuki,

T13958

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A;Reference number: 217834
A;Recession: T13958
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recession: T13958
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1166 <SUZ>
A;Cross-references: EMBL:AB016962; NID:d1261311; PID:d1038706; PIDN:CAB19493.1
A;Experimental source: strain Sprague Dawley
C;Genetics:
A;Gene: synGAP-b1

Query Match
Best Local Similarity 83.3%; Score 28; DB 2; Length 1166;
Best Local Similarity 83.3%; Pred. No. 2e+02;
MAtches 5; Conservative 1; Mismatches 0; Gaps 0;
MAtches 5; Conservative 1; Mismatches 0; Gaps 0;
Db 322 LNVKGK 6
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Db 322 LNVKGK 327

Search completed: December 14, 2000, 10:12:57
Job time: 150 sec
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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This SWISS-PROT entry between the Swiss In the European Bioinfor use by non-profit modified and this state entitles requires a lor send an email to 1 c	1	MEDLINE: 8934 MEDLINE: 8934 JOZÍASSE D.H.: Shaper N.L.: "Bovine alpha Characterizat Sequences in J. Biol. Chem -!- FUNCTION: ACCEPTOR N-ACETYL-	GATR_BOVIN STANDARD; p1476; O1-APR-1990 (Rel. 14, Cr O1-APR-1990 (Rel. 39, Le O1-APR-1990 (Rel. 39, Le N-ACETYLLACTOSAMINIDE AI (GALACTOSYLTRANSFERASE) D-GLUCOSAMINIDE ALPHA-1, GGTA1. BOS taurus (Bovine). Eukaryota; Metazoa; Chor Memmalia; Eutheria; Cete Bovidae; Bovinae; Bos.	7 L
SWISS-PROT een the Swi European Bio by non-pro fied and thi fies requir ties requir end an email	BETA-D-GALACTOSYL-1 COFACTOR: MANGANESE PATHWAY: GLYCOSYLATI SUBCELLULAR LOCATIO FORM IN TRANS CISTE DISEASE: AUTOIMMUNE PRODUCT). SIMILARITY: STRUCTU GLYCOSYLTRANSFERASE	, 893 e D.H e D.H alph eriza eriza eriza eriza eriza eriza eriza	1990 1990 2000 2000 SAMIN SAMIN SAMIN ELB; ELB; BOV	N N N N N N N N N N N N N N N N N N N
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01-NOV-1991 (Rel. 20, Last sequence update)
30-NAY-2000 (Rel. 3), Last annotation update)
N-ACETYLLACTOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE (EC 2.4.1.151)
(GALACTOSYLTRANSFERASE) (UDP-GALACTOSE:BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GUUCOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE).
GGTMA10R GGTA-1.
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send an email to license@isb-sib.ch).
           Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
Signal-anchor; Golgi stack; Alternative splicing; Manganese.
DOMAIN

1 41 CYTOPLASMIC (POTENTIAL).

TRANSMEM
42 60 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

DOMAIN
61 394 LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                               EMBL; M85153; AAA37711.1; -. pr.p. a2//17.
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"Mürine alpha 1,3 -galactosyltransferase.

spēcifies four isoforms of the enzyme by

J., Biol. Chem. 267:5534-5541(1992).

-1. FUNCTION: TRANSFER OF GALACTOSE FROM

ACCEPTOR MOLECULE (R)

-1- CATALYTIC ACTIVITY: UDP-GALACTOSE + B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leasen R.D., Rajan V.P., Ruff Cummings R.D., Lowe J.B.; "Isolation of a cDNA encoding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus, musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                          MGD;
                                                                                                                                                                                                                                                                                                                                          -1 COFACTOR: MANGANESE.
-1 PATHWAY: GLYCOSYLATION.
-1 SUBCELLULAR LOCATION: T
FORM IN TRANS CISTERNAE
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MEDLINE; 92184813.
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MEDLINE: 90046769.
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CARBOHYD
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UBPgalactose:beta-D-galactosyl-1,4-N-acetyl-D-glucosaminide
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INYL-R = UDP + ALPHA-D-GALACTOSYL-1,3-
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y alternative splicing.";
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VARSPLIC
SEQUENCE
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Daggett Garvin L., Hardies S.C.;
Daggett Garvin L., to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE LEUCINE, ISOL
VALINE, (THREONINE) TRANSPORT SYSTEM, WHICH IS ONE OF THE
PERIPLASMIC BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEMS OF
HIGH-AFFINITY TRANSPORT OF THE BRANCHED-CHAIN AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                 PFAM; PF01094; ANF_receptor; 1. PRINTS; PR00337; LEUILEVALBP.
                                                                                                                                                                                                                                                             EMBL; X58820; CAA41622.1;
PIR; S14619; S14619.
HSSP; P02917; 2LIV.
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15-JUL-1999
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01-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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nes 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNVKGK 6
                                                          ب
                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: PERIPLASMIC. SIMILARITY: BELONGS TO THE LEUCINE-BINDING PROTEIN FAMILY.
                                                          MNMKGK
                                                                              MNVKGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITER
                                                                                                   l Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                          an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria; gamma subdivision;
                                                                                                                                                       24
76
367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
394 AA;
                                                                                                                                                                                            transport; Transport; Periplasmic; 1 23 BY SIMILARITY.
                                                         σ
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 22, Last sequence up
(Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               freundii.
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                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                 23
367
101
39087 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319
35
62
46475 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN PRECURSOR
                                                                                                               90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                             MW;
                                                                                                    Score 28; DB Pred. No. 25; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                     agreement (See http://www.isb-sib.
                                                                                                                                                           LEU/ILE/VAL-BINDING PROTEIN BY SIMILARITY.; F731F36CB64CAC19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLONAC...) (POTE MISSING (IN SHORTER ISOFORM) R -> SPDGSFLATYHTK (IN SHORT 7766831640D1BBF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31;
Pred. No.
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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(LIV-BP).
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    371
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                                                                                                      0;
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                                                                                                                           Length 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 394;
                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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RESULT 5
ASPG_CAEEL
ID ASPG_CAEEL
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Best Local S
Matches 5
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CARBOHYD
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P50127;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sandrin M.S., Dabkowski P.L., Henning M.M., Mouhtouris McKenzie I.F.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 9510'
Strahan K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-YORKSHIRE; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-SPLEEN, AND LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 41:101-105(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               galactosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gustafsson K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence and chromosome localization of pig alpha 1,3
                                                                                                                        --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-ACETYL-D-GLUCOSAMINYL-R - UDP + ALPHA-D-GALACTOSYL-1,4
N-ACETYL-D-GLUCOSAMINYL-R - UDP + ALPHA-D-GALACTOSYL-1,3-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.
COFACTOR: MANGANESE.
PATRICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: GLYCOSYLATION.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: TRANSFER OF ACCEPTOR MOLECULE (R). CATALYTIC ACTIVITY: UE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: STRONG, TO BLOOD GROUP AB TRANSFERASE. SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOSYLTRANSFERASES.
                                                                                                                     MNVKGK
||||:
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L36535; AAA58775.1; -.
ferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                             Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95104914.
K.M., Gu F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
                                                                                                                                                                                                                                                                                                                           23
59
296
27
27
227
371
                                                                                                                                                                                                                                                                                                                                                                 Golgi stack; Glycoprotein; Transmembrane;

1 6 CYTOPLASMIC (POTENTIAL).

7 22 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

371 LUMENAL, CATALYTIC (POTENTIAL).

59 N-LINKED (GLCNAC. . .) (POTENTIAL).

296 N-LINKED (GICNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Golgi
                                                                                                                                                                                                                                                                                                                              227
43764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                               90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preece A.F.,
                                                                                                                                                                                                                                                                                                                                WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALACTOSE
                                                                                                                                                                                                             Score 28;
Pred. No.
1; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                              LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
SPEGSLEWIYQSK -> R (IN SHORT ISOFORM).
M -> I (IN REF. 2).
           PRT;
                                                                                                                                                                                                                                                                                                                              -> I (IN REF. 2).
CFC715E8D8993D4 CRC64;
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gustavsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM
           378
                                                                                                                                                                                                                                    26;
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                                                                                                                                                                                                                                                            Length 371;
                                                                                                                                                                                                                 Indels
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RESULT 6
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Best Local S
Matches 5
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01-NOV-1997;
01-NOV-1997;
30-MAY-2000;
                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGK_HORSE STANDARD; PRT; 4
P00559; P01-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
PHOSPHOGLYCERATE KINASE (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; PI
WORMPEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01:NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
PUTATIVE N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
(EC 3.5.1.26) (GLYCOSYLASPARAGINASE) (ASPARTYLGLUCOSAMINIDASE) (N4-(N-ACETYL-BETA-GLUCOSAMINYL)-L-ASPARAGINE AMIDASE) (AGA).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SIGNAL
Equus caballus (Horse)
Eukaryota; Metazoa; Ch
                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF01112; Asparaginase_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPRO00246;
                                                                                                                                                           327 MNVKGR
                                                                                                                                                                                  1 MNVKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U50198; AAA91260.1;
P20933; 1APZ.
                                                                                                                                                                                                          Similarity
5; Conser
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176
337
227
15
133
211
                                                                                                                                                                                                            Conservative
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41012
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361
227
15
133
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                                                                                                                                                                                                                                                                                                                                                                                                                      226
 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                      90.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oda; Chromadorea; Rhabditida; Rhabditoldea; Caenorhabditis.
                                                                                                                                                                                                                                                                       X
X
X
                                                                                                                                                                                                         Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                  GLYCOSYLASPARAGINASE, ALPHI
SIMILARITY).
GLYCOSYLASPARAGINASE, BETA
SIMILARITY.
BY SIMILARITY.
(GLCNAC. . .) (PO'
N-LINKED (GLCNAC. . .) (PO')
                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Lysosome; Signal.
                                                                                                416
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                                                                                                                                                                                                                                 Length 378;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
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Borzym K.,
Meitinger 1
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AGT_SITE
AGT_SITE
BENDING
SEQUENCE
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PUB; 2PGK;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Banks R.D., Blake C.C.F., Evans r.n., Blake G.C.F., Phillips A.W.;

"Sequence, structure and activity of phosphoglycerate legistence, structure and activity of phosphoglycerate legistence, and the sequence of the s
                                                                                                                                                                                                                                                                                                                                                             EEX. HUMAN STANDARD; PRT; 749 AA.

$\text{prisc} \text{2} \text{PRT}; \text{24} \text{24} \text{AA}.

$\text{prisc} \text{2} \tex
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MEDLINE: 82030789.

METRIM: 82030789.

METRIM: Structure of 3-phosphoglycerate kinase from The Transport of Cyanogen bromide peptides 656-CB14. Sequence of methionine-containing regions, sequence of the enzyme.";
                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
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DOMAIN
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                                                                                                                    Francis
                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSITE; PRO0477; PHGLYCKINASE.
                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSSUE-MUSCLE;
EDLINE; 79199779
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                                                                                                                                                                                                                                                                                             sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2PGK; 17-FEB-84.
   F., Strom T.M., Hennig S., Boeddrich A., Lorenz B., O., Mohnike K.L., Cagnoli M., Steffens C., Klages S., Pohl T., Oudet C., Econs M.J., Rowe P.S.N., Reinhardt er T., Lehrach H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001576; -. 0162; PGK; 1.
                                                                                                                                                                                                                             ; Metazoa;
Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                      Chordata;
Primates;
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1 ACETYLATION.
185 GLOBULAR DOMAIN 1
189 JOIN DOMAIN 1 6 2
1189 GLOBULAR DOMAIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEP IN THE SECO
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JOIN DOMAIN 1 & 2.

GLOBULAR DOMAIN 2.

ASSOCIATED WITH GLOBULAR DOMAI.

ALPHA-PHOSPHATE GROUP OF ADP-A:

PART OF SLOT FOR THE ADENINE RI

GLUCOSE OF ADP-ATP.
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: Pred. No. 29;
1; Mismatches
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                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
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29;
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CB1-CB4 and
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ADP-ATP.
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NINE RING.
NINE RING.
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ECONS M.J., Strom T.M., Meitinger T., Garabedian M., David Macher M.-A., Questiaux E., Popowska E., Pronicka E., Read Macher M.-A., Glorieux F.H., Direzner M.K., Hanauer A., Lehr Goulding J.N., O'Riordan J.L.H.;

"Distribution of mutations in the PEX gene in families with hypophosphataemic rickets (HYP).";

Hum. Mol. Genet. 6:539-549(1997).

-i- FUNCTION: PROBABLY INVOLVED IN BONE AND DENTIN MINERALI AND RENAL PHOSPHATE REABSORPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
Lipman M.
Karaplis
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Beck L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted [2]
                                                                                                                                                                                                                                                                                    VARIANTS HYP TYR-85; CYS-166; SER-25
MEDLINE; 97260404.
Holm I.A., Huang X., Kunkel L.M.;
"Mutational analysis of the PEX gene
hypophosphatemic rickets.";
Am. J. Hum. Genet. 60:790-797(1997).
                                                                                                                                                                                                                                                                                                                                                                                             "A gene (PEX) with homologies to endopeptidases is mupatients with X-linked hypophosphatemic rickets. The Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Francis F., Hennig S., Korn B., Reinhardt R., de Jong P., Poustka A., Lehrach H., Rowe P.S.N., Goulding J.N., Summerfield T., Mountford R., Read A.P., Popowska E., Pronicka Davies K.E., Oriordan J.L.H., Econs M.J., Nesbitt T., Drezner M.K., Oudet C., Pannetier S., Hanauer A., Strom T.M.,
                                                                                                                                                                                                                               VARIANTS HYP SER-77;
MEDLINE: 97252387.
Rowe P.S.N., Oudet C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grieff M., Mumm S., Waeltz
Thakker R.V., Schlessinger
"Expression and cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck L., Soumounou Y., Martel J., Krishnamurthy G., Goodyer C.G., Tenenhouse H.S.; Pex/PEX tissue distribution and evidence for a dele region of the Pex gene in X-linked hypophosphatemic J. Clin. Invest. 99:1200-1209(1997).
                                                                               -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PR-!- TISSUE SPECIFICITY: LYMPHOCYTE AND FETAL
                                                                                                                                                                                                                                                                                                                                                                                  Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meindl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4-641 FROM MEDLINE; 96024647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Meitinger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and sequencing of human PEX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
BRAIN, PLACENTA, SKELETAL MUSCLE, AND PANCREAS; NOT IN ADULT AND FETAL HEART, LUNG, LIVER, AND KIDNEY.
DISEASE: DEFECTS IN PEX ARE A CAUSE OF X-LINKED HYPOPHOSPHATEMIC RICKETS (HYP), A DOMINANT DISCRDER CHARACTERIZED BY IMPAIRED PHOSPHATE UPTAKE IN THE KIDNEY, WHICH IS LIKELY TO BE CAUSED BY ABNORMAL REGULATION OF SODIUM PHOSPHATE COTRANSPORT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 97343443.
Quarles L.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.C
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Soumounou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FEB-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing of human PEX from a bone cDNA library:
its developmental stage-specific regulation in
                                                                                                                                                                                                                               Oudet C.L.,
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                                                                                                                                                                                                                                                            PRO-138; LEU-534 AND
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                                                                                                                                                                                                                                Francis F., Sinding C.,
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D.;
the
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                                                                    TAL BRAIN;
PANCREAS;
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                                                                                                                                                                families with X-linked
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                                                                    (POTENTIAL).

NOT IN ADULT

NOT IN ADULT
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EMBL: Y10196; CAA71258.1; EMBL: U875645; AAB47749.1; EMBL: U87284; AAB47762.1; EMBL: U87284; AAB47562.1; CAA62926.1; J CAA69926.1; J CAA69926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.isb-sib.ch/ann or send an email to license@isb-sib.ch).
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                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                       Hydrolase;
                                                                                                                                                                                                                                                                                                  PFAM; PF01431; Peptidase_M13;
                                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO00130; -.
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SIMILARITY: BELONGS TO
METALLOPROTEASE); ALSO
                                                                                                                                                                                                                                                                                                                                                                                           U81182; AAB42219.1; JOI
AB000712; AAB51604.1;
AAC50552.1;
                                                                                                                                                                                                     pR00786; NEPRILYSIN.

; PS00142; ZINC_PROTERSE; 1.

se; Metalloprotease; Aminopeptidase; Zinc; Glycoprotein;

se; Metalloprotease; Aminopeptidase; Dinc; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                        Disease mutation.
CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II
(POTENTIAL).
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                                                                                                                                                    MEMBRANE PROTEIN)
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p70669; p97439;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
METALLORIDOPEPTIDASE HOMOLOG PEX (EC 3.4.24.-) (PHOSPHATE REGULATING NEUTRAL ENDOPEDTIDASE) (X-LINKED HYPOPHOSPHATEMIA PROTEIN) (HYP)
(VITAMIN D-RESISTANT HYPOPHOSPHATEMIC RICKETS PROTEIN).
PEX OR PHEX OR HYP.
               Strom T.M., Francis F., Lorenz B., Lehrach H., Meitinger T.; Lehrach deletions in Gy and Hyp X-linked hypophosphatemia."; Hum. Mol. Genet. 6:165-171(1997).
                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
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                                                               SEQUENCE FROM N.A. MEDLINE; 97217775.
                                                                                         Du L., Desbarats M., Viel J., Glorieux F.H., Cawthorn C., Ecarot "CDNA cloning of the murine Pex gene implicated in X-linked hypophosphatemia and evidence for expression in bone."; Genomics 36:22-28(1996).
                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 96411643.
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SEQUENCE FROM N.A
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Rodentia;
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G -> R (IN HYP).
/FTId=VAR_006745.
/FTId=VAR_006746.
A -> D (IN REF. 6).
W -> A (IN REF. 6).
W -> A (IN REF. 6).
G -> A (IN REF. 6).
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C -> S (IN HYP).

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C -> Y (IN HYP).

/FTId=VAR_006739.

/FTId=VAR_006740.

R -> C (IN HYP).

FTIG=VAR_006741.

F -> C (IN HYP).

/FTIG=VAR_006742.

M -> I (IN HYP).
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Pred. No. 51;
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                                                     В.,
                                                                                                                                                                                                                                                                                                                                                    Mismatches
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EMBL; U73910; AAC25964.1; --
EMBL; U73913; AAC25964.1; --
EMBL; U73913; AAC25965.1; --
EMBL; U73914; AAC25966.1; --
EMBL; U73911; AAC25963.1; --
EMBL; U73915; AAC35967.1; --
EMBL; U75646; AAB47750.1; --
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Goodyer C.G., Tenenhouse H.S.;
                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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INTERPRO; IPR000130; -
INTERPRO; IPR000718; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pex/PEX tissue distribution and evidence for a region of the Pex gene in X-linked hypophosphate J: Clin. Invest. 99:1200-1209(1997).
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632 LNVKGK 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PROBABLY INVOLVED IN BONE AND DENTIN MINERALIZATION AND REMAL PHOSPHATE REABSORPTION.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: BONE.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
                                                                                                                             Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soumounou Y., Martel J., Krishnamurthy
                                                                                                                                                                                                                                                                                                                                                                                                                    Metalloprotease;
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D -> V (I
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Pred. No. 51;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
ZINC (CATALYTI
                                                                                                                                                                                                                                                                                                      PROTON
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A88FA481C376C18A CRC64;
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(CATALYTIC) (BY SIMILARITY).
DN DONOR (POTENTIAL).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 37, Last annotation update)
FIBROBLAST GROWTH FACTOR I) (XEFGF-1).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                          FGFA_XENLA P48805;
            Development 114:711-720(1992).

-i- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.

-i- SUBCELLULAR LOCATION: SECRETED (PROBABLE).

-i- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMI
                                                                                                        inducing factor for mesoderm
specification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEAM; PEO0276; Ribosomal_L23; 1.

PROSITE; PS00050; RIBOSOMAL_L23; FALSE_NEG.

Ribosomal protein; rRNA-binding.

SEQUENCE 98 AA; 11411 MW; 22F5448F3DE2BB0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 92315916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Whinkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and tl
                                                                                                                       Isaacs H.V., Tannahill D., Slack J.M.W.; "Expression of a novel FGF in the Xenopus embryo. A new candidate inducing factor for mesoderm formation and anteroposterior
                                                                                                                                                                                                                   Xenopodinae;
                                                                                                                                                                                                                                 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-MADRID E;
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-!- SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondria
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30-MAY-2000 (Rel. 39,
505 RIBOSOMAL PROTEIN
                                                                                                                                                    [saacs H.V.,
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            BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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Best Loc
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MEDLINE; 92315916.
ISAACS H.V., Tannahill D., Sla.
"Expression of a novel FGF in inducing factor for mesoderm for specification.";
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INTERPRO: IPR002348: -.
PFAM: PF00167: FGF: 1.
PRINTS: PR00262: ILLHBGF.
PRINTS: PR00263: HBGFFGF: 1.
PROSITE: PS00247: HBGFFGF: 1.
Growth factor: Mitogen: Signal.
SIGNAL
                                                  EMBL; X62594; CAA4448
HSSP; P09038; 1BFF:
INTERPRO; IPR002209;
INTERPRO; IPR002248;
PFAM; PF00167; FGF; 1
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Ol-FEB-1996 (Rel. 33, Last sequence update)
Ol-FEB-1996 (Rel. 33, Last annotation update)
FIBROBLAST GROWTH FACTOR-4-II PRECURSOR (FGF-4-II) (HBGF-4-II)
(EMBRYONIC FIBROBLAST GROWTH FACTOR II) (XEFGF-II).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibba; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGFB_XENLA
P48806;
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                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                               Development 114:711-720(1992).

-!- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
-!- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
-!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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83.3%;
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in the Xenopus embryo. A new
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FIBROBLAST GROWTH FACTOR-4-I.
AAE63D65E82AD1BD CRC64;
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Landlick R., Oxender D.L.;
"The complete nucleotide sequences of the Escherichia coli LIV-BP LS-BP genes. Implications for the mechanism of high-affinity branched-chain amino acid transport.";
J. Biol. Chem. 260:8257-8261(1985).
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J. Cell.
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P02917; P76698;
21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
LEU/ILE/VAL-BINDING PROTEIN PRECURSOR
                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                    coli
                                                                                                                                                                                                                                                            Adams M.D., Wagner L.M., Graddis T.J., Landick R., Anton
Gibson A.L., Oxender D.L.;
"Nucleotide sequence and genetic characterization reveal
essential genes for the LIV-I and LS transport systems o
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 86086153. Antonucci T.K., La
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SEQUENCE OF 24-35.
STRAIN-K12 / EMG2;
MEDLINE; 97443975.
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Sofia H.J., Burland V.,
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                                                                                       Ovchinníkov Y.A.,
                                                                                                               STRAIN-K1
                                                                                                                                              Sofia H.J., Burland V., Daniels D.L., Plu
"Analysis of the Escherichia coll genome.
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                   MEDLINE;
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                                                      primary structure of a Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                            nucci T.K., Landick R., Oxender D.L.; leucine binding proteins of Escherichia coli as models for leucine binding proteins of Escherichia coli as models for ying the relationships between protein structure and functional biochem. 29:209-216(1985).
                                                                              H.N.;
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                                             78:313-316(1977).
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FIBROBLAST GROWTH FACTOR-4-II.
JB0180BB8824E3B3 CRC64;
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(LIV-BP).
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EMBL: J05516; AAA83881.1; -.
EMBL: M29377; AAA24075.1; -.
EMBL: U00039; CAB34662.1; ALT_INIT.
EMBL: BECO0422; AAC76485.1; ALT_INIT.
PIG: A03415; BLEC.
PIG: A03415; A37074.
RJB: A37074; A37074.
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***EDELINE; 89199638.

**EDELINE; 89199638.

**SECK J.S., Saper M.A., Quiocho F.A.;

**SECK J.S., Saper M.A., Quiocho F.A.;

**SECRETION: Since the leucine of the leucine of the leucine of the leucine/isoleucine/valine-binding protein and its semiplex with leucine.

**J. Mol. Biol. 206:171-191(1989).

**J. Mol. B
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#RAIN=KIZ / W3110;
#Wutiger S., Hughes G.J., Pa
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WESS-2DPAGE; P02917; COLI.
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gomparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
pectrophoresis 18:1259-1313(1997).
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LEUILEVALBP.
port; Transport;
Pasquali C., Hochstrasser D.F.;
he SWISS-PROT data bank.
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RESULT 13
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P05655; P70984;
P01-NOV-1988 (Rel. 09, Created)
Ol-NOV-1988 (Rel. 09, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
LEVANSUCRASE PRECURSOR (EC 2.4.1.10) (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
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Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
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Fouet A.,
                   STRAIN=168 / PY79;
MEDLINE; 84178454.
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  Arnaud
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RESULT 14
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Matches 4; Conser
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EMBL; Z94043; CAB08015.1; -.
EMBL; K01987; AAA22724.1; -.
EMBL; X02730; CAA26513.1; -.
EMBL; Z99121; CAB15450.1; -.
PIR; A25040; A25040.
PIR; S07309; S07309.
                                                                                                                                                                                                                                         Q08462:
01-OCT-1994 (Rel. 30, Created)
01-OCT-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ADENYLATE CYCLASE, TYPE II (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
(ADENYLYL CYCLASE) (FRAGMENT).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sucrose and regulation of the steady-state mRNA level by sacU sacQ genes.";
J. Bacteriol. 168:380-388/1997
            Stengel D., Parma J., Gannage M.-H., Barouki R., Hanoune J.;
"Different chromosomal localization expressed in human brain.";
Hum. Genet. 90:126-130(1992).
                                                                                                                                                                                                                                                                                                                                                  CYA2_HUMAN
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SIGNAL
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                                                                                                                                                                         Mammalia;
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CATALYTIC ACTIVITY: SUCROSE + (2,6-BET GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1)
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SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES
FUNCTION: THIS
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52971
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66.78;
MEMBRANE-BOUND,
                                                                                 Gannage M.-H.,
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V -> I (IN REF. 3).
; 3FBF2F571B41D5B0 CRC64;
                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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P46743;
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                                            MEDLINE: 94180393.

Wolff G., Plante I., Lang B.F., Kueck U., Burger G.;

"Complete sequence of the mitochondrial DNA of the chlorophyte alga-
Prototheca wickerhamii. Gene content and genome organization.";

J. Mol. Biol. 237:75-86(1994).

-i- SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X74210; CAA52
EMBL; L21993; AAA64
HSSP; P26769; 1AB8.
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                                                                                                                                                             Chlorellaceae;
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                                                                                                                                    SEQUENCE FROM N.A.
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                                   -!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS
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ENZYME REGULATION: INSENSITIVE TO CA(2+)/CALMODULIN. STIMULATED B
THE G PROTEIN BETA AND GAMMA SUBUNIT COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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PS00452; GUANYLATE_CYCLASES;
AMP synthesis; Transmembrane;
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(Rel. 32, Last annotation)
AL RIBOSOMAL PROTEIN S4.
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AAA64923.1; -.
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CYTOPLASMIC (POTENTIAL).
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Glycoprotein; Duplication
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    Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q9t1w8 cyanidium c
Q59163 pyrococcus
Q9ycr2 aeropyrum p
Q5925 salmonella
Q3925 salmonella
Q9yr57 drosophila
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301	23		7	erycoprocein.	3 ;;	••	GLYCOSYLTRANSFERASES.	RITY: ST	RITY: STI	N TRANS	LULAR LOC	DATHWAY: GLYCOSYLATION.	OSYL-1,4	,-D-GLUCOS	TIC ACTIV	LE (R).	ON: TRANS	gy 4:193	enzyme."	transfera	the minin	., Mache	94331837.	TROM N	Eutheria	Metazoa		GALACTOS	TOSE: BET!	LTRANSFER	8 (TremBLrel.	_	7 (TrEMBLrel.	FRELLMINARI		
301	376	;	22 0	ירפדווי.	Glycosyltransferase;	1587.1; -	ERASES.	STRUCTURAL	RONG, TO	DISTERNAE	SUBCELLULAR LOCATION: TYPE	SYLATION.	-N-ACETYL	SAMINYL-R	/ITY: UDP		FUNCTION: TRANSFER OF GALACTOSE	-201(1994		ise: stru	nal size	: B.A., A			•			LTRANSFE	1-D-GALAC	PASE)	rel 08,	rel. 02,		LINANT		
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01-MAY-2000;
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**Partic Pathogen Helicobacter pylori.**;

**Pathogen Hel
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MEDLINE; 99120557.
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ENTATIVE TRANSCRIPTIONAL REGULATOR.
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     PRELIMINARY;
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OS9163
OS9163;
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Oh.
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO02028; -.
INTERPRO; IPRO03009; -.
PFAM; PF00290; trp_syntA; 1.
PROSITE; PS00167; TRP_SYNTHASE_ALPHA;
Hypothetical protein; Chloroplast.
SEQUENCE 266 AA; 29344 MW; E56B7FI
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"Reconstruction of the ancient red algal plastid genome:
gene repertoire, and syntemy.";
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Score 28; DB
Pred. No. 1.4e
1; Mismatches
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                                                    DB 1;
1.4e+02;
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Best Local Similarity
Matches 5; Conser
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Best Local
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                                                                                                     fragment containing a Salmonella path minutes on the chromosome map of Salm typhimurium LT2."; chiqurium LT2."; infect. Immun. 66:3365-3371(1998). EMBL; AF060869; AAC26653.1; ... INTERPRO; IPR000150; ... INTERPRO; EPS01228; COF_1; UNKNOWN_1. Hypothetical protein. SEQUENCE 463 AA; 49218 MW; D62AD0
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01-NOV-1998
01-JUN-2000
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MEDLINE: 99310339.

MEDLINE: 99310339.

MENDLINE: 99310339.

MENDLINE: 99310339.

MENDLINE: Ankai A., Kosugi Jin-no K., Takahashi M., Sekine M., Baba S., Ankai A., Kosugi Jin-no K., Takahashi M., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K., Kubota K., Nakamu Nomura N., Sako Y., Kikuchi H.;

"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Ki.";

DNA Res. 6:83-101(1999).

EMBL; AP000061: BAA80185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999
01-NOV-1999
01-MAY-2000
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MEDLINE;
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31 LNVKGK 36
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         MNVKGK 6
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MNVRGK 422
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8 (TrEMBLrel. 08, Las
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AL 49.2 KDA PROTEIN.
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(TIEMBLrel. 13, Last annotation update)
L 52.0 KDA PROTEIN APEll99.
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Last annotation updat
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                                          Score 28; DB 2; L0
Pred. No. 1.8e+02;
1; Mismatches 0;
                                                                                                        D62AD07F6375E428 CRC64;
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                                                                                                                                                                                                                                                                                                          subdivision;
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1.8e+02;
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                                               Indels
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035812;
01-JAN-1998
01-JAN-1998
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Q9VZP5;
Q1-MAY-2000
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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EMBL: AJ001637; CAA04890.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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PF01431; Peptidase_M13; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE;
SEQUENCE 749 AA; 86305 MW; 69
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pred. No. 2
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DR FYBBSE; FB90007457: CG10840.

DR INTERPRO; IPR0007957: -.
                    Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

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Pterygota;
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Pred. No. 3.5e+02;
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Dugan - Rocha
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    B.C., Dunn P.
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RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
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RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McIntosh D.R., Nelson N.V., Mobary C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nussern D.R., Peacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Glubs R.A., Myers E.W., Rubin G.M., Venter J.,
RA Glubs R.A., Myers E.W., Rubin G.M., Venter J.,
RA Glubs R.A., Myers E.W., Rubin G.M., Venter J.,
RA Glubs R.A., Myers E.W., Rubin G.M., Venter J.,
RA Science 287:2185-2195(2003).
DR EMBL, AE003605, AAF52033.1.
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PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
SEQUENCE 1135 AA; 124718 MW; 8BA760EEEE45E9DA CRC64;
                                                                                                                                                                                                                                                                                       PFAM; PF00169; PH; 1. PFAM; PF00616; RasGAP; 1
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EMBL; AF050183; AAC40082.1;
INTERPRO; IPR001849; .
INTERPRO; IPR001936; -.
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Pred. No.
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Pred. No. 4.3e+02;
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at Associates with the
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EMBL: AB016962: CAB19493.1; -.
INTERPRO: IPRO01849; -.
INTERPRO: JPR001936; -.
INTERPRO: JPR001936; -.
PFAM: PF00169: PH; 1.
PFAM: PF00616: RasGAP: 1.
PFAM: PF00517E: PS50003: PH_DOWAIN: 1.
PROSITE: PS50018: RAS_GTPASE_ACTIV_2: 1.
SEQUENCE 1166 AA; 127744 MW; 5804EE4
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09QWL2;
01-MAY-2000
01-MAY-2000
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SYNGAP-B1.
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Q9UGE2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Q1570F3.1 (HOMOLOG OF THE RAT SYNAPTIC RAS GTPASE-ACTIVATING PROTEIN
                                                                                                                                                                         PFAM; PF00169; PH; 1.

PFAM; PF00616; RASGAP; 1.

PROSITE; PS50003; PH_DOMAIN; 1.

PROSITE; PS50018; RAS_GTPASE_ACTIV_2;

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SEQUENCE 1179 AA; 129242 MW; E7C31
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Submitted (DEC-1999) to the
EMBL; ALO50332; CAB63778.1;
INTERPRO; IPRO01849; -.
INTERPRO; IPRO01936; -.
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OJ570F3.1.
Homo sapiens (Human).
Homosapiens (Human).
Homota; Metazoa; Chordata;
Horria; Primates;
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
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    424 LNVKGK 429
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Pred. No. 4.4e+02;
1; Mismatches (
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Pred. No. 4.4e+02;
l; Mismatches 0
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Abstr. - Soc. Neurosci. 1466:1-1(0).
EMBL: AF058789; AAC63510.1; -.
EMBL: AF048976; AAC63510.1; -.
INTERPRO; IPR001849; -.
INTERPRO; IPR001936; -.
PFAM; PF00169; PH; I.
PFAM; PF00616; PH; I.
PFAM; PF00616; PH; I.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS500018; RAS_GTPASE_ACTIV_2; 1.
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Kim J.H., Liao D., Lau L.-F.
"SynGAP: a Synaptic RasGAP t
Protein Family.";
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SYNGAP-B.
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Kim J.H., Liao D., La
"SyngAP: a Synaptic F
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EMBL; AF058790; AAC63511.1;
INTERPRO; IPR001849; -.
INTERPRO; IPR001936; -.
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PFAM; PF00616; RASGAP; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
SEQUENCE 1249 AA; 137357 MW; DC549FCF1624BDBA CRC64;
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c RasGAP that Associates with the
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Pred. No. 4.7e+02;
1; Mismatches 0;
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Sciurognathi; Muridae;
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Best Local Similarity 83.3%
Matches 5; Conservative
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STRAIN-MCAN/FR/82/PHAROAH;
STRAIN-MCAN/FR/82/PHAROAH;
MAUGLIOI I.L., Howard M.K., Stothard J.R., Miles M.A.;
Mauglioli I.L., Howard M.K., Stothard donovani complex.";
"Genomic diversity in the Leishmania donovani complex.";
"Genomic diversity in the EMBL/GenBank/DDBJ databases.
"Genomic diversity in the EMBL/GenBank/DDBJ databases."
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Lijigaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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21856 MW; 63468A7C174972EC CRC64;
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Post-processing: Minimum Match 0%
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    A_Geneseq_36:*

1: /SIDS1/gcgda*

2: /SIDS1/gcgda*

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2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT: *
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Compugen Ltd
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5.688 Million cell updates/sec
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pred. No. is the number of results predicted by chance to be score greater than or equal to the score of the result being and is derived by analysis of the total score distribution. to have a being printed,

SUMMARIES

12	10987654	ω ω Ρ	Result
26 26	2222222	28 27 27	Score
89.7 89.7	93.1 93.1 89.7 89.7 89.7 89.7 89.7	96.6 93.1	Query Match
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W71250 Y68661	W97388 Y56504 R78382 Y82505 R60610 R67755 R78388	W03548 W97389 Y56505	ID
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ALIGNMENTS

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RESULT
ORF-2 protein sequence from BamHI fragment of HVT
                                        21-APR-1997
                                                                              W03548;
                                                                                                                  W03548 standard; Protein; 185 AA.
                                      (first entry)
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Herpes virus of turkey; open reading frame; ORF; homology; vector; avian herpes virus; recombinant viral vaccine; intergenic region; IBDV; cytomegalovirus immediate early promoter; UL55 gene; repeat region; ILTV; antigen; infectious bursal disease virus; Marek's disease virus; MDV; infectious laryngotracheitis virus; avian anaemia virus; vaccination; infectious bronchitis virus; IBV; poultry; Gumboro disease; WPI; 1996-364150/37. N-PSDB; T39309. Audonnet JCF, Laplace ELF, 30-DEC-1994; 03-JUL-1996. EP719864-A2. (INMR) RHONE MERIEUX SA. 28-DEC-1995; Herpesvirus of turkey. Newcastle disease. Bublot MJM, Riviere MAE; 94FR-0016017 95EP-0402970 Darteil RJ, Duinat CV; ILTV;

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Best Local
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                                                                                                                                                                                                                                                                                                                               aromatic amino acid synthesis; vaccine; bacterial infection; otitis media; conjunctivitis; pneumonia; bacteremia; sinusit pleural empyema; endocarditis; meningitis.
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and l
         New polynucleotides and polypeptides of the 5-enolpyruvylshikimate-3-phosphate synthase familthe creation of a vaccine against, and diagnosis
                                                                                                   Brown
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                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded
                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   W97389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W97389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVVKGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant avian vaccine having sequence encoding as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                              1999-214154/18
DB; X15931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|||
mvikgk 118
                                                                                                   JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 1;
                                                                                                   Chalker AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                         pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                     97US-0896345
                                                                                                                                                                              97US-0896345
                                                                                                                                                                                                                                                                                                                                                                                                by the aroA
                                                                                                                                                                                                                                                         /note= "Xaa= not specified"
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.6%;
83.3%;
                                                                                                   Payne DJ,
especially
                                                                                                                                                                                                                                                                                                                                                                                                ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB
Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises herpes virus as vector genic polypeptide inserted between
                                                                                                   Shilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                       family
                                                                                                   ĽX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 185;
           and
                                                                                                    Traini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                               sinusitis;
                         useful
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                         ĺ'n
             of.
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RESULT
Y56505
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthase (aroA) open reading frame (ORF). The aroA product converts shikimate-3-phosphate to 5-enolpyruvoylshikimate-3-phosphate. Inhibition of this reaction prevents the synthesis of aromatic amino acids, p-aminobenzoate acid (a precursor of folate) and ubiquinone. The polypeptides or their variants are useful for assessing aroA expression and genetic variation, the creation of a vaccine and the diagnosis and treatment of bacterial infection, especially S. pneumoniae and the diseases otitis media, conjunctivitis, pneumonia, bacteremia, sinusitis
                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae; aroA; antimicrobial; antik diagnosis; detection.
                                                                                                                        Polynucleotide sequences encoding Streptococcal 5-enolpyruvylshikimate-3-phosphate synthase enz screening candidate antibacterial compounds -
                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y56505
                                                                                                     Disclosure;
                                                                                                                                                                                                  Payne
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                                                                                                                                                                                                                                                      18-JUL-1997;
                                                                                                                                                                                                                                                                         15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pleural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                              18-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::|||
| 353 miikgk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVVKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence
                                                                                                                                                                            2000-000099/01.
                                                                                                                                                                                                 'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                      SMITHKLINE SMITHKLINE
                                                                                                                                                                                                  Chalker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                    Page 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columns 11-12; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                       pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae aroA
                                                                                                                                                                                                                                                                         98CA-2237786
                                                                                                                                                                                                                                                      97US-0896354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endocarditis
                                                                                                                                                                                                 AF,
                                                                                                                                                                                                                      BEECHAM CORP
BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.1%;
                                                                                                    43pp;
                                                                                                                                                                                                                                                                                                                                                                     antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is encoded by the 5-enolpyruvylshikimate-3-phosphate
                                                                                                                                                                                                 Shilling
                                                                                                                                                                                                                                                                                                                                                                     5-enolpyruvylshikimate-3-phosphate oacterial; vaccine; immune response:
                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    ORF protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20,
1.3e+02;
                                                                                                                                                                                                   Traini CM,
                                                                                                                            enzýmes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 415;
                                                                                                                                                                                                   Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                     useful
                                                                                                                                                                                                                                                                                                                                                                      response;
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                                                                                                                                                                                                                                                                                                                                                                                                     NO:4.
                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                               synthase;
                                                                                                                                                                                                                                                                                                                                                                       infection;
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The present sequence is 5-enolpyruvylshikimate-3-phosphate synthase (aroA) isolated from Streptococcus pneumoniae. AroA polynucleotides and protein may be used in the diagnosis, prevention and treatment of diseases associated with the expression of aroA. For example, the polynucleotide and aroA proteins may be used to treat disorders associated with decreased aroA expression. AroA polynucleotides may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of aroA by expressing inactive proteins or to supplement the patients own production of aroA proteins.

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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulate aroA expression by binding with the ceils own aroA genes and preventing their expression. They may also be used to study the expression and function of aroA proteins and their role in cellular metabolism. The aroA proteins may then be used as antigens in the production of antibodies against aroA and in assays to identify medulators (agonists and antagonists) of aroA expression and activity. The anti-aroA antibodies and aroA antagonists may also be used to down regulate aroA expression and activity. They may be used in this way to treat diseases caused by Streptococcus pneumoniae. The anti-aroA antibodies may also be used as diagnostic agents for detecting the presence of aroA polypeptides in samples (e.g. by enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-enolpyruvylshikimate-3-phosphate synthase; aroA; aromatic amino acid synthesis; vaccine; bacterial infection; otitis media; conjunctivitis; pneumonia; bacteremia; sinusitis;
The present sequence represents a 5-enolpyruvylshikimate-3-phosphate synthase designated aroA. The aroA product converts shikimate-3-phosphate to 5-enolpyruvoylshikimate-3-phosphate. Inhibition of this reaction prevents the synthesis of aromatic amino acids, p-aminobenzoate acid (a precursor of folate) and ubiquinone. The polypeptides or their variants are useful for assessing aroA expression and genetic variation, the creation of a vaccine and the diagnosis and treatment of bacterial infection, especially S. pneumoniae and the diseases otitis media,
                                                                                                                                                                                       New polynucleotides and polypeptides of the S-enolpyruvylshikimate-3-phosphate synthase family the creation of a vaccine against, and diagnosis at Streptococcal infection, especially in meningitis
                                                                                                                                                                                                                                                                              WPI; 1999-214154/18
N-PSDB; X15930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-enolpyruvylshikimate-3-phosphate synthase designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W97388 standard; Protein; 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conversely, antisense nucleic acid molecules may be administered to down regulate arch expression by binding with the cells own arch genes and
                                                                                                                                                         Claim 1; Columns 9-8; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pleural empyema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
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353 miikgk 358
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nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVVKGK 6
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                                                                                                                                                                                                                                                                                                                               Chalker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                 97US-0896345.
                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0896345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endocarditis;
                                                                                                                                                                                                                                                                                                                               AF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
66
                                                                                                                                                                                                                                                                                                                               Payne DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                            Shilling LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
1.3e+02;
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                                                                                                                                                                                                         and treatment of
                                                                                                                                                                                                                                                                                                                               Traini CM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aroA
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RESULT
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 (aroā) isolated from Streptococcus pneumoniae. Aroa polynucleotides and control of aroa polynucleotides and control of aroa polynucleotide and aroa proteins may be used to treat disorders control of aroa proteins may be used to treat disorders control of aroa proteins may be used to treat disorders control of aroa proteins may be used to treat disorders be control of aroa proteins aroa proteins or deletions in a control of aroa proteins or to supplement the patients own production of aroa proteins. Conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely, antisense nucleic acid molecules may be administered to down conversely antisense and function of aroa proteins and their role in cellular metabolism. The aroa proteins may then be used as antigens in the converse of a milbodies and antisense and aroa antisense in the converse of a milbodies and antisense of aroa proteins and antisense of a molecules may also be used to down converse of antibodies and activity. They may liso be used to down converse of antised by Streptococcus pneumoniae. The anti-aroa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conjunctivitis, pneumonia, bacteremia, sinusitis, pleural empyema, endocarditis and especially meningitis.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 13; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide sequences encoding Streptococcal s-enolpyruvylshikimate-s-phosphate synthase enz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; 238851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Payne DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ]::/||
365 miikgk 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVVKGK
                                                                                                                                                                                                                                                                                                                                   present sequence is 5-enolpyruvylshikimate-3-phosphate oA) isolated from Streptococcus pneumoniae. AroA polynuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antimicrobial; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                 candidate antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chalker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0896354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98CA-2237786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shilling LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Traini CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                     enzymes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                         synthase
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e 9d

used as diagnostic

agents

for detecting

the

RESULT Y82505

Y82505 standard; protein; 187 AA.

12-JUL-2000 Y82505;

(first entry)

밁 Ş

1 MVVKGK 6 :||||| 3 lvvkgk 8

Best Local Similarity
Matches 5; Conserv

Conservative

83.3%;

Pred.

ed. No. 30; Mismatches

0

Indels

0,

Gaps

0

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RESULT: 6
DIXAK BARRAR ARKER ARKER
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                                                                                   This sequence represents a truncated tobacco mosaic virus (TMV) completed by a frame shift my fement protein. This sequence is produced by a frame shift in the produced to the 30 end of both strands of a HindIII site at viral position of a BamHI/KpnI fragment of TMV. The nucleotides AGCT are interoduced to the 30 end of both strands of a HindIII site at viral position of This leads to the production of an in-frame stop codds causing production of the 64 residue protein, rather than the wind type 267 amino acid protein. The resulting protein is non-functional and viruses containing it cannot spread from one plant functional and viruses containing it cannot spread from one plant could be used in the method of the invention for the overproduction of meterologous proteins. The method is esp. used for the production of peptides which cause an antigenic response in mammals, partic. for use in viral vaccines, for for generating a contraceptive immune response. The infectious clones may encode coat proteins for other plant viruses, or proteins conferring protection against insects and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Overprodn. of heterologous peptide in plants via tobacco mosaic vitsus infection - in which the coat protein gene is modified by insertion of heterologous sequence, partic. for producing viral antiquens for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thincated; tobacco mosaic virus; TMV; movement protein; coat protein; frame shift; mutation; in-frame stop codon; antigen; mammal; v@gal vaccine; contraceptive; immune response; plant virus; insect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          presence of aroA polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 98; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beachy RN, Fitchen JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09521248-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Truncated TMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 movement protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0192477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US01467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.1%;
66.7%;
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Wickham TJ,

Kovesdi I,

Roelvink PW,

Bruder

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(GENV-) GENVEC

INC.

11-SEP-1998; 28-MAY-1999; 10-SEP-1999; 23-MAR-2000 WO200015823-A1

98US-0099851 99US-0136529 99WO-US20728 Human adenovirus type

15

infection;

Adenovirus; adenoviral; Ad; fibre knob; fibre protein; gene therapy; Human adenovirus type 15 fibre knob protein sequence SEQ ID NO:11.

Recombinant fiber protein used for creating vectors for delivering desired gene to a cell with minimal ectopic infection, comprises an amino terminus of an adenoviral fiber protein and a trimerization

an

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The present invention describes a recombinant fibre protein (I) comprising an amino terminus of an adenoviral fibre protein and a trimerisation domain. The trimerisation domain comprises: (a) an adenoviral fibre knob domain having a mutation affecting at least one amino acid residue within the region corresponding to the AB loop, B sheet, DE loop or FG loop of the wild-type adenovirus (Ad) 5 fibre
Sequence
                                                                                                                                           Example
         exemplification of
                                                                                                                                           <u>ب</u>
187
                                                                                                                                           Fig 1; 69pp; English.
                                                                                                                  least one
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Query, Match

89.7%;

Score 26;

DB 16;

Length

64;

Sequence

64

A

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RESULT
R67755
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                                                                                밁
8XB
                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                        A transcriptional vector comprises in a 5'-3' direction (1) a 5' non-transcribed region of tobamovirus, (11) a replicative enzyme of tobamovirus, (11) a foreign gene connecting region, and (1v) a 3' non-transcribed region of tobamovirus. The vector also has a transcriptional promoter region upstream of the tobamovirus region and a transcriptional terminator region downstream of the tobamovirus region, neither of which is recognised by the host cell, a replication initiation site which functions in the host cell, and a selective marker gene. This sequence is the tobamovirus movement (sic) protein and the sequence is the tobamovirus construct (See Q71546) which in turn was used in the constructional vectors pL5013 and pL5020.
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27-28; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                             Improved transcriptional vector of plant virus - pL5013 and pL5020 which are prepd. and mass produtested for stability and function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobamovirus movement protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R60610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R60610 standard;
                      R67755 standard; Protein; 264 AA.
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobamovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||||
40 lvvkgk 45
                                                                              1 MVVKGK 6
:|||||
3 lvvkgk 8
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q71546.
                                                                                                                                                                                        264 AA;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tobacco mosaic virus; vector; transcription; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93JP-0297704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 264
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                         89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26;
Pred. No.
1; Mismatc
                                                                                                                             Score 26; DB
Pred. No. 1.4e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replication site; ori; coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       prant virus - esp. and mass produced,
                                                                                                                           DB 15; Lc. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                    Length 264;
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                                                                                                                               Indels
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                                                                                                                               Gaps
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RESULT 10
R78388
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Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                A chimeric cucumber mosaic virus RNA-3 (given in Q76108) has the coat protein gene replaced by a gene encoding an elicitor, TOMV P30, having the sequence given in R67755. The construct elicits a minus-sense RNA that interacts with the RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-resistance on a host plant, e.g. tobacco, tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA constructs for imparting pathogen, esp. virus, resistance to plants - encodes RNA that interacts with viral RNA polymerase to generate an eliciting agent.
                                                Truncated; tobacco mosaic virus; TMV; movement protein; coat protein; frame shift; mutation; in frame stop codon; antigen; mammal; primer; viral vaccine; contraceptive; immune response; plant virus; insect; polymerase chain reaction; PCR; amplify.
                                                                                                                                        17-APR-1996
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 36; 50pp; English.
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N-PSDB; Q76108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De HAAN PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANO ) SANDOZ LTD.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUNGEN VERW GES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomato mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1995
                                                                                                               Tobacco mosaic virus movement protein.
                                                                                                                                                                                           R78388 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1994
                        Pobacco mosaic virus
                                                                                                                                                                                                                                                         :|||||
3 lvvkgk
                                                                                                                                                                                                                                                                                 1 MVVKGK 6
                                                                                                                                                                                                                                                                                                           Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                           264 AA;
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94WO-EP01817
                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                       89.7%;
                                                                                                                                                                                             268
                                                                                                                                                                                                                                                                                                           Score 26; DB Pred. No. 1.4e 1; Mismatches
                                                                                                                                                                                                                                                                                                            1.4e+02;
ches 0;
                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                                                                                                    Length 264;
                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 11
W71250
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                             Overprodn. of heterologous peptide in plants via tobacco mosaic virus infection - in which the coat protein gene is modified by insertion of heterologous sequence, partic. for producing viral
29-DEC-1993;
30-DEC-1992;
                                              US5811653-A.
                                                                                     Protein sequence of the specification
                                                                                                                W719250;
                    30-DEC-1993;
                                 22-SEP-1998
                                                                       Replicon; plant transformation system; tobamovirus;
                                                                                                   20-NOV-1998
                                                                                                                             W71250 standard; Protein; 268
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                     protection
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 118-119;
                                                                                                                                                                                                                                                                                                                                                                      ant#gens for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                            Beachy RN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-EEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST
                                                                                                                                                             :|||||
3 lvvkgk 8
                                                                                                                                                                          1 MVVKGK 6
                                                                                                                                                                                                                                                                                                                                                                                                              1995-283768/37
                                                                                                                                                                                                                                     against
                                                                                                                                                                                                                        268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Fitchen JH;
                                                                                                                                                                                        Conservative
                                                                                                   (first entry)
93US-0176414.
92US-0997733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9405-0192477
                    93US-0176414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US01467
                                                                                                                                                                                                                                     insects
                                                                                                                                                                                             89.7%;
                                                                                                                                                                                                                                                                                                                                                         157pp; English.
                                                                                                                                                                                                                                     and
                                                                                                                                                                                        1;
                                                                                                                                                                                             Score 26; DB 16;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                     diseases.
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                    Length 268;
                                                                                                                                                                                        Indels
                                                                                                                                                                                        0;
                                                                                                                                                                                       Gaps
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RESULT
Y68661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence appears in the specification, which describes a CC plant transformation system which comprises a replicon and a helper CC virus. The replicon comprises a tobamovirus replication origin, at least CC virus. The replicon comprises a tobamovirus protein and a gene encoding a non-tobamovirus gene encoding a non-tobamovirus protein and a gene CC tobamovirus replicase. The helper virus is a tobamovirus that has a gene concoding a tobamovirus replicase but lacks a functional gene encoding the concoding a tobamovirus replicase but lacks a functional gene encoding the composition of the protein protein. DNA encoding the replicon is integrated as CC a transgene into a chromosome of a tobamovirus susceptible plant cell. The plant transformation system is useful for producing the con-tobamovirus protein by integrating the replicon DNA into a chromosome CC of a plant cell and infecting the plant cell with the helper virus so that the protein is expressed and accumulates in the plant cell. The protein produced can be a regulatory enzyme or a structural, regulatory or therapeutic protein, e.g. an interleukin or colony-stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                             New chimaeric adenoviruses containing a genome adenovirus serotypes, useful in gene therapy -
                                                                                                            Havenga
                                                                                                                                                                          08-JUL-1998;
                                                                                                                                                                                                         08-JUL-1999;
                                                                                                                                                                                                                                      20-JAN-2000
                                                                                                                                                                                                                                                                     WO200003029-A2.
                                                                                                                                                                                                                                                                                                                               Chimaeric adenovirus; gene therapy; antigenicity; serotype 39; penton protein; hexon protein.
                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of the fiber protein of Adenovirus serotype 39
                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                              Y68661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y68661 standard; Protein; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 19-22; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant transformation system - comprises replicase-deficient tobamovirus vector and movement-protein-deficient helper virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-530986/45
                                                                                                                                         (INTR-) INTROGENE BY
                                                                                                                                                                                                                                                                                                     Adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOS-) BIOSOURCE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
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3 lvvkgk 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVVKGK 6
                                                                            2000-171149/15
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268
                                                                                                          Vogels R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                        98EP-0202297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AΑ;
                                                                                                                                                                                                         99WO-NL00436
                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%;
83.3%;
                                                                                                            Bout A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB
Pred. No. 1.4e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                 derived from different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 268;
                                                                                                                                                                                                                                                                                                                                                  fiber protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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0;

Example 2; Fig

7; 92pp; English

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RESULT
Y68664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 5
Y68642-70 represent the amino acid sequences of the fiber proteins of Adenovirus serotypes 8, 9, 13, 14, 20, 23, 24, 25, 27, 28, 29, 30, 32, 33, 34, 35, 36, 37, 38, 39, 42, 43, 44, 45, 46, 47, 48, 49 and 51. The proteins are used in the course of the invention to construct chimaeric adenoviruses with reduced antigenicity. The chimaeric adenoviruses comprise at least part of a fiber protein of an adenovirus serotype providing the chimaeric virus with a desired host range and at least part of a penton or hexon protein from another, less antigenic, serotype. The chimaeric adenoviruses are useful for gene therapy, especially where repeated delivery is required. Adenoviruses of the
                                                                                                                                                                                                                                                                                                                                                                                                      New chimaeric adenoviruses containing a genome derived from different adenovirus serotypes, useful in gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serotype 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of the fiber protein of Adenovirus serotype 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y68664 standard; Protein; 341 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-171149/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INTR-) INTROGENE BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 83.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVVKGK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenovirus; gene therapy; antigenicity;
44; penton protein; hexon protein.
                                                                                                                                                                                                                                                                                                                                            Fig 7; 92pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vogels R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98EP-0202297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-NL00436
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83.38;
                                                                                                                                                                                                                                                                                                                                                English.
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Pred. No. 1.8e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Query Match Best Local Similarity

89.7%; 83.3%;

Score Pred.

No :

DB 21; 1.8e+02;

Length

Sequence

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RESULT 14
Y68668
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                          CC of Adenovirus serotypes 8, 9, 13, 14, 20, 23, 24, 25, 27, 28, 29, 30, CC of Adenovirus serotypes 8, 9, 13, 14, 20, 23, 24, 25, 27, 28, 29, 30, CC 32, 33, 34, 35, 36, 37, 38, 39, 42, 43, 44, 45, 46, 47, 48, 49 and 51. CC The proteins are used in the course of the invention to construct continues comprise at least part of a fiber protein of an adenovirus denoviruses comprise at least part of a fiber protein of an adenovirus construct part of a penton or hexon protein from another, less antigenic, CC serotype providing the chimaeric virus with a desired host range and at CC least part of a penton or hexon protein from another, less antigenic, CC serotype. The chimaeric adenoviruses are useful for gene therapy, CC especially where repeated delivery is required. Adenoviruses of the invention are useful can be constructed to have a desired host range and CC a diminished capability to raise neutralizing antibodies, an absence of, CC or decreased infection of, antigen presenting cells of the immune system CC (e.g. macrophages), and an ability to escape trapping in the liver or through increased target cell specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a diminished capability to raise neutralizing antibodies, an absence of, or decreased infection of, antigen presenting cells of the immune system (e.g. macrophages), and an ability to escape trapping in the liver through increased target cell specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimaeric adenovirus; gene therapy; antigenicity; fiber protein: serotype 48; penton protein; hexon protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention are useful can be constructed to have a desired host range a diminished capability to raise neutralizing antibodies, an absence
                                                                                                                                                                                                                                                                                                                      Example 2;
                                                                                                                                                                                                                                                                                                                                                        New chimaeric adenoviruses containing a genome derived from different adenovirus serotypes, useful in gene therapy .
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Havenga M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200003029-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of the fiber protein of Adenovirus serotype 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y68668 standard; Protein; 343
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198 lvvkgk 203
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5; Conserv
                                                                                                                                                                                                                                                                                                                        Fig 7; 92pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vogels R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA;
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bout
                                                                                                                                                                                                                                                                                                                      English.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ore 26; DB 21;
ed. No. 1.8e+02;
Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 341;
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                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                            Query Watch 89.7
Best Pocal Similarity 83.7
Matches 5; Conservative
                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVVKGK 6
:|||||
199 lvvkgk 204
                                                                                                                                                                                                                                                                                                                                                                                Chimaeric adenovirus; gene therapy; antigenicity; fiber protein; sexotype 45; penton protein; hexon protein.
                                                                                                                                                                                                                                            New Chimaeric adenoviruses containing a genome derived from different agenovirus serotypes, useful in gene therapy .
                                                                                                                                                                                                                                                                                                       08-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Y68,665;
                                                                                                                                                                                                                                                                                                                                                                                                                                              v68665 standard; Protein;
                                                                                                                                                                                                                                Example 2; Fig 7; 92pp; English.
                                                                                                                                                                                                                                                                   WP項 2000-171149/15.
                                                                                                                                                                                                                                                                                Hawenga M, Vogels R,
                                                                                                                                                                                                                                                                                                                         08-50UL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      Aṃino acid sequence of the fiber protein of Adenovirus serotype 45
                                                                                                                                                                                                                                                                                          (TNTR-) INTROGENE BV.
                                                                                                                                                                                                                                                                                                                                        20-ŪAN-2000.
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                                                                                                                                                                                                                                                                                                                                                                  Adenovirus
                                   * :|||||
203 lvvkgk 208
                                             11 MVVKGK 6
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                                                                                                    345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                             98EP-0202297.
                                                                                                                                                                                                                                                                                                                          99WO-NL00436.
                                                                       89.7%;
                                                                                                                                                                                                                                                                                Bout A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                Score 26; DB 21; Length 345; Pred. No. 1.8e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                 0,
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                                                                 Gaps
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                              Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
    164575 segs, 16761186 residues
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Gapop 10.0 ,
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US-08-896-345-2
US-08-687-559-3
US-08-553-619B-7
US-08-176-1414B-2
US-08-749-903-1
US-08-749-903-3
US-08-749-903-5
US-08-749-903-5
US-08-749-903-5
US-08-749-903-5
US-08-946-329A-95
US-08-946-329A-96
US-08-946-528-9
US-08-946-528-9
US-08-946-528-9
   US-08-173-497-3

US-08-286-889-3

US-08-485-618-3

US-08-362-652-3

US-08-605-672-3
                                                                         US-08-990-114-3
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Sequence 4, Appli
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Sequence 25, Appli
Sequence 3, Appli
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Sequence 5, Appli
Sequence 9, Appli
Sequence 95, Appli
Sequence 95, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
ENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-896-345-4
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US-08-896-345-4
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                                                Query Match
Best Local S
Matches 4
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Patent No. 5883239
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: P500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chalker, Alison Franch APPLICANT: Traini, TITLE OF INVENTION: NOVEL aroa NUMBER OF SEQUENCES: 4
    1 MVVKGK 6
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/896,345 FILING DATE:
                                                                                                                                                                                                                                       TELEFAX: 609-520-3259
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                                                 Conservative
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US-08-943-363-3
US-08-947-451-16
US-08-594-447-12
US-08-541-964-11
US-08-655-647-26
US-08-468-5768-14
US-08-468-5778B-14
US-08-468-578B-14
US-08-468-578B-14
US-08-468-578B-14
US-08-468-578B-14
                                                Score 27; DB pred. No. 96; 2; Mismatches
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Sequence 16, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 26, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 35, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 1, Appli
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Sequence: Title: Perfect score:

Scoring table:

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US-08-896-345-2
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Matches 4; Conserv
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                                                                                                                                                                       GENERAL INFORMATION:
                                                                                       APPLICANT: Fitchen, John H.
APPLICANT: Beachy, Roger N.
TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
NUMBER OF SEQUENCES: 30
                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                 365 MIIKGK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastsEQ for Windows Version 2.0 IRRENT APPLICATION DATA: RPPLICATION NUMBER: US/08/896,345 FILING DATE: GLASSIFICATION: 530 FOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                               1 MVVKGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 427 amino acid TYPE: amino acid STRANDEDNESS: sir
COUNTRY:
                                             ADDRESSEE: fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bloom, Allen 29,135 EEGISTRATION NUMBER: 29,135 EEGERENCE/DOCKET NUMBER: P51 EECOMMUNICATION INFORMATION: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORNEY/AGENT INFORMATION:
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ZIP: 08543
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UENCE CHARACTERISTICS:
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BER OF SEQUENCES: 4
RESPONDENCE ADDRESS:
DDRESSEE: Dechert Price & Rhoads
TREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICANT: Chalker
LICANT: Traini,
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              La Jolla
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                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERBNCE/DOCKET NUMBER: 137-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/687,559
FILING DATE: No. 5955647ember 18, 19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01467
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
             TELEFAX: 415/85
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 619-678-5070
                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
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                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                             STREET: 975 Call
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nes 5; Conserv
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                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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N FOR SEQ ID NO:
CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   CA
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                               415/857-1125
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VENTION: Virus Resistant Plants
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83.3%;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-553-619B-7
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Best Local Similarity
Thes 5; Conserv
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                                                                US-08-687-559-25
                                                                                 RESULT
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Best Local Similarity bo...
Thes 5; Conservative
Sequence 25 Application US/08687559 Patent No. 5955647 GENERAL INFORMATION:
APPLICANT: Fitchen, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 2, Application US/08176414B vatent No. 5811653
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01 FILING DATE: 29-Dec-1993 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: US/11/17 Albert D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turpen, Thomas H.
TITLE OF INVENTION: VIRAL AMPLIFICATION OF RECOMBINANT
TITLE OF INVENTION: MESSENGER RNA IN TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington D.C.
STATE: District of Columbia
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Halluin, Albert P. REGISTRATION NUMBER: 25,227
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                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                              3 LVVKGK 8
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amino acid
                                                                                                                                                                                                                                                                                                                                         268 amino acids
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1299 Pennsylvania Avenue, N.W.
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Pred. No. 1e+02;
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1.1e+02;
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US-08-749-903-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08749903 Patent No. 5759812
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein IMMEDIATE SOURCE: CLONE: TMV MPwt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beachy, Roger N.
TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: POT/US95/01467
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                                                                                 APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN SELENIUM-BINDING PROTEIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: No. 5
CLASSIFICATION: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 013-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Learn, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4225 Executive Square, CITY: La Jolla
                                                                                                                                        COUNTRY:
                                                                                                                                                                          STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                             STATE:
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                                                                                                                         ZIP: 94304
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LVVKGK 8
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                                                                                                                                            SD
                                                                                      Diskette
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5955647ember 18,
US/08/749,903
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Pred. No. 1.1e+02
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ILING DATE: Filed Herewith APPLICATION DATA:

PLICATION NUMBER:

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# MOLECULE TYPE: NO

# MOLECULE TYPE: NO

# INMEDIATE SOURCE:

# CEONE: 989953

US-08-749-903-1
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US-08-749-903-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIDE APPLICATION NUMBER: US/08/7/
FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :y Match
t Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FALING DATE:
TALING DATE:
TOTAL STREET INFORMATION:
TOTAL STREET STREET STREET
THE STREET STRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | MVVKGK 6
| :|||||
| LVVKGK 381
ECULE TYPE:
                                                                                                                                                                                           MATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPUTER: IBM Compatible pERATING SYSTEM: DOS OFFWARE: FastSEQ Version 1.5 RENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUTER READABLE FORM:
EDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OUNTRY: U
IP: 94304
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                                                          SICANT: Bandman, Olga
CANT: Hawkins, Phillip R.
BE OF INVENTION: NOVEL HUMAN SELENIUM-BINDING PROTEIN
BER OF SEQUENCES: 5
ESPONDENCE ADDRESS:
DRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                            EFERENCE/DOCKET NUMBER: PFECOMMUNICATION INFORMATION: 215-855-0555
                                                                                                                          NGTH: 472 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHONE:
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GOMMUNICATION INFORMATION:
EEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNEY/AGENT INFORMATION:
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GISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,ING DATE:
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Pred. No. 1
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RESULT 10 US-08-749-903-5

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                                         Query Match
Best Local Similarity
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; LIBRARY: GenBank
; CLONE: 374792
US-08-749-903-3
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US-08-749-903-4
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                                                                                                                           US-08-749-903-4
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Best Local Similarity 83...
5; Conservative
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                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 227630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
376 LVVKGK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 LVVKGK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 94304
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CITY: Palo Alto
                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                          1 MVVKGK 6
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVVKGK 6
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                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                           amino acid
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                                                        Conservative
                                                                                                                                                                                              single
linear
                                                                                                                                                                                   peptide
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                                                                     89.7%;
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                                                                                                                                                                                                                                                                                                                              PF-0163 US
                                                                     Score 26; DB 1;
Pred. No. 1.8e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 1;
Pred. No. 1.8e+02;
                                                        Mismatches
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                                                                                 Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                             squence 11, Application US/08772270A
tent No. 6019984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: S1ng
TOPOLOGY: linear
MOLECULE TYPE: pepti
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 298710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,903
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILTMS NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0163 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                   APPLICANT: ROSENDAL, SOTEN
TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN SELENIUM-BINDING PROTEIN
                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                            APPLICANT: Ricciatti, Paul
APPLICANT: Mallard, Bonnie
                                                                                                                                                                                                                              APPLICANT: MacInnes, Janet
                           STREET: 40 King
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                            376 LVVKGK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Versior
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CITY: Palo Alto
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              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                            1 MVVKGK 6
                                                                                     NDDRESSEE:
                                                                                                                                                                                                                                                INFORMATION:
M5H 3Y2
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                                                                  40 King Street
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                                                                                     Bereskin & Parr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 1;
Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 472;
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US-08-772-270A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 6580
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEPAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino acids
                               COMPUTER: IN PC COMPATIBLE
COMPUTER: IN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10500
FILING DATE:
CLASSIFICATION:
DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/972,229
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
RAME: KOTMAN, Alan S.
REGISTRATION NUMBER: 33,932
REGISTRATION NUMBER: 33,932
REGISTRATION NUMBER: 19603/00001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-853-8104
TELEPHONE: 716-853-8104
TELEFAX: 716-853-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9310500
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,270A
FILING DATE: December 23, 1996
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: Alan S. K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: Recombinant Vaccine For Procine
TITLE OF INVENTION: Pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578 LVVKGK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 14202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Buffalo
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear LECULE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1600 Empire Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 3.8e+02;
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0S-08-9
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US-08-946-329A-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                  APPLICATION NUMBER: 60/061,323
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 08/729,743
FILING DATE: 10-JUL-1996
APPLICATION NUMBER: 08/567,357
BILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349,498
APPLICATION NUMBER: 08/349,498
APPLICATION TOPPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: R
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                   ©OMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 4225 EX
SITY: La Jolla
STATE: CA
                                                                              PELEPHONE: 619/678-5070
PELEFAX: 619/678-5099
PEMATION FOR SEQ ID NO: 95
SQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.7%;
Local Similarity 83.3%;
hes 5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ©RGANISM: Actinobacillus pleuropneu STRAIN: Serotypes 2, 3, 4, 6 and 8 INDIVIDUAL ISOLATE: Swine CELL TYPE: Gram negative bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: dou
M@POLOGY: linear
G:329A-95
                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/946,329A
FALLING DATE: 07-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICANT: Beachy, Philip A. LICANT: Porter, Jeffrey A
                                                                                                                                                  AME: Haile, Lisa A.
EGISTRATION NUMBER: 38,347
EFERENCE/DOCKET NUMBER: 07
ECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
                                                                93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1244 amino acids
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                 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
                                                                                                                                                                       07265/140001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Pred. No. 4.4e+02;
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RESULT 15
US-08-946-528-5
; Sequence 5, Application US/08946528
; Patent No. 5958746
. GENERAL INFORMATION:
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US-08-946-329A-96
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Best Local Similarity 83...
""" hes 5; Conservative
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619/67 INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/061
FILING DATE: 07-007-1996
APPLICATION NUMBER: 08/729
FILING DATE: 10-UUL-1996
APPLICATION NUMBER: 08/567
FILING DATE: 04-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NO NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beachy, APPLICANT: Porter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4
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                                                                                                                                                                                      Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/140001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/946,329A FILING DATE: 07-OCT-1997
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                           1 MVVKGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                            8 VVVKGK 13
                                                                                                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Fish & Richardson P.C. 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                       99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: 08/349,498
02-DEC-1994
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, Jeffrey A.
                                                                                                                                                                                                   86.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/567,357
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                                                                                                                                                                                                  Score 25;

    Mismatches

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                                                                                                                                                                                                                  Length 99;
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APPLICANT: Hilman, Jennifer L.
APPLICANT: Bidmmeneige
APPLICANT: CALLY NOIL
APPLICANT: CALLY NOIL
APPLICANT: CALLY NOIL
APPLICANT: CALLY NOIL
TITIE OF INVENTION: BISCTRON TRANSPORT PROTEINS

NUMBER OF SCOUNTES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Invyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
STRIE: CA
COUNTER: USA
COUNTER: BAJA04
COMPUTER: BAJA04
COMPUTER: BAJA04
COMPUTER: APPLICATION DISACTE:
MEDIUM TYPE: DISACTE:
COMPUTER: INCOMPATION
COURTER READABLE FORM:
MEDIUM TYPE: DISACTE:
COMPUTER: INCOMPATION:
MEDIUM TYPE: DISACTE:
COMPUTER: INCOMPATION:
APPLICATION NUMBER: US/08/946.528
FILLING DATE: Filed Herewith
APPLICATION NUMBER: US/08/946.528
FILLING DATE: THE HERMATION:
APPLICATION NUMBER: US/08/946.528
FILLING DATE: SITUANDER:
FILLING DATE: THE HERMATION:
APPLICATION NUMBER: US/08/946.528
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                                                  December 14, 2000, 10:12:57; Search time 27.57 Seconds
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(without alignments)
13.811 Million cell updates/sec
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Title: Perfect score: Sequence: US-09-051-034A-13 29 MVVKGK 6

Scoring table: BLOSUM62 Gapop 10.0 ,

182106 seqs, 63460219 residues Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

182106

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_65:* pir1: * pir3: * pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

29	2) i	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	Ф	7	o	σ	4	ω	2	⊷	Result
22		J E	S	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	27	27	28	29	29	Score
Ö	٥	n :	7	9	9	9	9	89.7	9	٥	89.7	9	89.7	9	٩	89.7	89.7	89.7	89.7	89.7	89.7	89.7	9	89.7	ω.	ω.		.0	100.0	Query Match
178		0 0	87	1581	1504	1052	1049	815	493	472	472	371	367	346	333	302	268	268	267	264	264	264	161	100	662	633	σ	327	183	Length
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77857	604092	0000	528800	T30832	A33602	B49219	S51784	E70021	S63060	G01872	S27878	S32664	S32663	C81446	T05121	S40714	S26359	WMTM30	JC1339	WMBVL2	WMBVL1	WMBVT3	T37236	R5EC23	T20570	G71026	G70413	T06602	C69474	₽
NADH denyarogenase	THOO SOMET PROCEED	101010	n	pentafunctional en	DNA-directed DNA p	toxin III - Actino	toxin III - Actino	3-hydroxyacyl-CoA	ct	selenium-binding p	selenium-binding p	fiber protein - hu		О		hypothetical prote		30K protein - toba	movement protein -		30K protein - toma	protein - tom	probable H+-transp	ribosomal protein	hypothetical prote	hypothetical prote		hypothetical prote	conserved hypothet	Description

A; Map

position:

Query Match Best Local Similarity

100.0%;

Score 29; Pred. No.

DB 24; N

Length 327;

C;Genetics:
A;Gene: ATSP:F16J13.20

ALIGNMENTS

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Conserved hypothetical protein AF1796 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: C69474
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A; Accession: C69474
A, Accession: C69474
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C69474
                                                                                                                                             R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15789
A;Accession: T06602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-183 <KLE>A;Cross-references: GB:AE000979; GB:AE000782; NID:g2689302; PID:g2648766; TIGR:AF1796 C;Superfamily: conserved hypothetical protein MJ1247
A;Molecule type: DNA
A;Residues: 1-327 <BEV>
A;Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.20
A;Experimental source: cultivar Columbia; BAC clone F16J13
                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                 hypothetical protein F16J13.20 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999 C;Accession: T06602
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Best Local Similarity
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100.0%; Pred. No. 14;
tive 0; Mismatches
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A; Status prezental DNA A; Molecule type: DNA A: Residues: 1-633 < KAW>
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A;Crossizeferences: GB:AP000006; NID:g3236133; PIDN:BAA30615.1; A;Experimental source: strain OT3
A;Note: Enis accession replaces an interim accession for a seque C;Genetas:
C;Genetas:
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G71026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein PH1507 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 17-Mar-2000 C;Accession: G71026
R;Kawagebayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamo! M; Ohituku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida DNA Res; 5, 55-76, 1998
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Best Local Similarity
Thehes 5; Conserv
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A:Title The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666
A;Accession: G70413
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-162 <AQF>
A;Cross***Geferences: GB:AE000734; NID:g2983733; PIDN:AAC07301.1; PID:g2983740; GB:A;Experimental source: strain VF5
C;Genetigs:
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C;Supertamily: NADH dehydrogenase (ubiquinone) chain
C;Keywords: membrane-associated complex; NAD; oxidore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoJ1 - Aquifex aeolicus C;Species Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999 C;Accession: G70413
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                                                                                                                                                                                                    ;Superfamily: unassigned ATP-binding;Keywords: ATP;Keywords: ATP;438-628/Domain: ATP-binding cassette
                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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83.3%;
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Pred. No.
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ed. No. 1.3e+02;
Mismatches 0;
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Kushida,
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                                                       A;Experimental source: strain K12
R;Arnold, R.J.; Reilly, J.P.
Anal. Biochem. 269, 105-112, 1999
A;Title: Observation of Escherichia coli ribosomal proteins
A;Reference number: A59071; MUID:99196679
A;Reference number: A59071; MUID:99196679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .A.; Rose, D.J.; Mau, Z.; 997
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F08A8.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to C;Accession: T20570 R;Harris, B.
A; Contents: annotation; mass spectrographic analysis A; Note: no post-translational modifications were observed C; Genetics:
                                                                                                                                                                                                                       A;Cross-references: GB:X02613; NID:g42825; PIDN:CAA26462.1; PID:g534975 A;Note: translation of initiator Met is not shown; the initiator overlap R;Wittmann-Liebold, B.; Greuer, B.
FEBS Lett. 108, 69-74, 1979
A;Title: Primary structure of protein L23 from the Escherichia coli ribc A;Reference number: A02814; MUID:80092111
                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 13, 4521-4526, 1985
A;Title: Structure of the Escherichia coli
A;Reference number: A23129; MUID:85242118
A;Accession: D23129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribosomal protein L23 [validated] - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 28-Feb-1980 #sequence_revision 31-Oct-1997 #text_change 28-Jan-2000
C;Accession: A65125; D23129; A02814
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
A; Introns: 38/3; 102/2;
C; Superfamily: acyl-CoA
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R;Harris, B.
submitted to the EMBL Data
submitted to umber: Z19294
                                                                                                                                                                A; Molecule type: protein A; Residues: 1-79,81-100 <WIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Zurawski, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-100 <BLAT>
A;Residues: 1-100 <BLAT>
A;Cross-references: GB:AE000408; GB:U00096; NID:g1789694;
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: A65125
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A; Residues: 1-662 <WIL>
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A;Accession: T20570
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                    A;Residues:
                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown;
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66.7%;
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Pred.
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No.
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1.4e+02;
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                       in mass spectrographic anal
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jok protein - tomato mosaic virus (strain L)
C;Specles: tomato mosaic virus
A;Note: host (tomato)
C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_C
C;Accession: A04182
R;Takamatsu, N.; Ohno, T.; Meshi, T.; Okada, Y.
Nucleic Acids Res. 11, 3767-3778, 1983
A;Title: Molecular cioning and nucleotide sequence of the A;Reference number: A93473; MUID:83220776
A;Accession: A04182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Map position: IV
C:Superfamily: vacuolar H+-transporting ATPase 16K chain
C:Keywords: ATP; hydrogen ion transport; hydrolase; trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable H+-transporting ATPase (EC 3.6.1.35) chain Vha3, vacuolar - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000 C:Accession: T37236; T37270 R:Oka, T.; Yamamoto, R.; Futai, M. J. Biol. Chem. 272, 24387-24392, 1997 A:Title: Three vha genes encode proteolipids of Caenorhabditis elegans vacuolar-type ATF A;Reference number: Z21636; MUID:97450964 A;Accession: T37236
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C;Superfamily: Escherichia coli ribosomal protein
C;Keywords: protein biosynthesis; ribosome
F;1-100/Product: ribosomal protein L23 #status exp
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WMBVT3
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A;Molecule type: mRNA
A;Residues: 1-161 <OKA>
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C;Complex: large subunit ribosomal proteins: L1 (PIR:R5EC1), L3 (PIR:R5EC3), L2 (PIR:R5E
(PIR:R5EC11), L13 (PIR:R5EC13), L14 (PIR:R5EC14), L15 (PIR:R5EC15), L16 (PIR:R5EC16), L1
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A; Residues: 1-161 <OK2>
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A; Title: Nucleotide sequence analysis of the movement genes of resist A; Reference number: JQ1456; MUID:92113565
A; Reference number: JQ1457
A; Recession: JQ1457
A; Rolecule type: genomic RNA
A; Residues: 1-264 <CAL>
A; Residues: 1-264 <CAL>
A; Note: the authors translated the codon TGG for residue 68 as Cys C; Comment: This protein is involved in cell-to-cell transport of the C; Superfamily: tobravirus 30K protein
C; Keywords: DNA binding; transport protein
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A; Residues: 1-264 <CAL>
A; Nesidues: the authors translated the codons TGG for residue 68 as Cys,
A; Note: the authors translated the codons TGG for residue 68 as Cys,
C; Comment: This protein is involved in cell-to-cell transport of the
C; Superfamily: tobravirus 30K protein
C; Keywords: DNA binding; transport protein
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A; Residues: 1-264 <TAK>
C; Superfamily: tobravirus 30K
C; Keywords: DNA binding
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N;Alternate names: transport protein
C;Species: tomato mosaic virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1
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C;Date: 31-Dec-1992 #sequence_revision
C;Accession: JQ1457
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R;Calder, V.L.; Palukaitis, P.
J. Gen. Virol. 73, 165-168, 19
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Pred. No. 1e+02;
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A.Experimental source: strain OM
R.Goeles, P.; Lomonossoff, G.P.; Butler, P.J.G.; Akam, M.E.; Gait, M.J.; Karn, Proc. Natl. Acad. Sci. U.S.A. 79, 5818-5822, 1982
A.Title, Nucleotide sequence of tobacco mosaic virus RNA.
A.Reference number: A93926; MUID:83299880
A.A.Coession: A93926
A.Residues: 1999: genomic RNA
A.Residues: 1-179, N',181-224, N',226-227, N',229-231, V',233-259, A',261-268
A.Cross-references: GB:V01409; NID:g62125; PIDN:CAA24689.1; PID:g663265
A.Experimental source: strain Vulgare
A.Note: the sequence contains proteins 27.9K (residues 20-268), 25.3K (43-268)
C:Superfamily: tobravirus 30K protein
  30K protein - tobacco mosaic virus (;Speckes: tobacco mosaic virus, TMV C;Darekes: tobacco mosaic virus, TMV C;Darekes: p25.Feb-1,924 #sequence_revision 10-Nov-1995 #text_change 07-May-1999 C;Accessing, S26359 C;Accessing, S26359 R;Koh, H:K.; Song, E.K.; Lee, S.Y.; Park, Y.I.; Park, W.M.
                                                                                                                  RESULT
S26359
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C;Date: 18-Aug-1982 #sequency 18-Aug-1982 #text_change 23-Jul-1999
C;Accession: A91965; A93926; A04181
R;Meshi/T: Ohno, T: Okada, Y.
J. Blockem. 91, 1441-1444, 1992
A;Title: Nucleotide sequence and its character of cistron coding for the 30
A;Reference number: A91965; MUID:82239259
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C:Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-May-1997
C:Accession: JC1339
R:Yu, X:: Zhu, Y:: Ying, H.: Chen, Z.
Chinese,J. Biotechnol. 12, 211-214, 1996
A:Title: Molecular cloning, nucleotide sequencing and plant transformation A:Reference number: JC1339
A:Accession: JC1339
A:Accession: JC1339
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A; Residues: 1-268 <MES>
A; Cross greferences: GB: V01407;
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C; Keywords:
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A; Resiques: 1-267 < YUA>
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83.3%;
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Pred. No. 1e+0
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Pred. No. 1e+02;
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A; Experimental so
C; Genetics:
A; Map position: 4
A; Note: F7H19.80
                                                                                                                                                                  hypothetical protein F7H19.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05121
R;Bevan, M; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancr submitted to the Protein Sequence Database, July 1998
A;Reference number: Z15399
A;Rocession: T05121
A;Molecule type: DNA
A;Residues: 1-333 < BEV>
A;Residues: 1-333 < BEV>
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C;Genetics:
A;Introns: 141/2; 207/1; 286/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein R10E11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #te
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                                                                                                                                                    A; Cross-references:
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A; Residues: 1-268 < KOH>
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A;Title: Nucleotide sequence of cDNA of the tobacco mosaic virus
A;Reference number: $26358; MUID:93065219
A;Accession: $26359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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Search completed: December 14, 2000, 10:13:00
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FIBP_TMVOM
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SBP1_HUMAN
SBP1_MOUSE
SBP2_MOUSE
YNL9_YEAST
RT31_ACTPL
RT32_ACTPL
RT32_YEAST
ARO1_PNECA
YI74_BURCE
RL23_ACTAC
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TAL_ANASP
AROA_STRIN
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P02424 escherichia
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P03584 tobacco mos
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Query Match
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This SWISS-PROT entry is copyright. It is p between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit Institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to licenseeisb-sib.ch). EMBL; AE000979; AAB89472.1; TIGERRO; IPRO01347; PFAM; PF01380; SIS; 1. Hypothetical protein. SEQUENCE 183 AA; 20147 MW; FC2B8DA78E2E	30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 48-40-40 (Rel. 39, Last annotation update) 48-41-40 (Rel. 39, Last annotation update) 49-58 (Rel. 39, Las	24 82.8 147 1 RL2B_CAEEL ALIGNMENTS ALIGNMENTS 196_ARCFU STANDARD; PRT; 183 AA. 128478; DAMY-2000 (Rel 39 Created)	35 25 86.2 411 1 RR1_SPIOL 35 25 86.2 457 1 PCAK_ACICA Q43975 36 25 86.2 484 1 ATPB_SYNCLE 37 25 86.2 484 1 ATPB_SYNCLE 38 25 86.2 787 1 RELA_MYCLE 39 25 86.2 787 1 RELA_MYCTU Q49640 39 25 86.2 790 1 RELA_MYCTU Q50638 40 25 86.2 894 1 WPRA_BACSU P54423 41 25 86.2 950 1 IF2_LACLA 42 25 86.2 15112 1 PHYE_ARATH 43 25 86.2 1634 1 DPOL_METJA Q58295 44 24 82.8 139 1 LAMP_DETMA P33575
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Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
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30-MAY-2000 (Rel. 39, Created)
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Bacteria; Firmicutes;
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                                                                                                                                                             Du W.,
                                                                                                                                                                                                                                                                                                                 Streptococcus
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SEQUENCE 381 AA; 42117 M
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PROSITE; PS00958; TRANSALDOLASE_2;
PROSITE; PS01054; TRANSALDOLASE_1;
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the zwf region of the
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01-MAR-1992
30-MAY-2000
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MEDLINE; 85242118.
Zurawski G., Zurawski S.M.;
Tructure of the Escherichia coli S10
Structure of the Escherichia coli S10
Nucleic Acids Res. 13:4521-4526(1985).
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PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
Aromatic amino acid biosynthesis; Transferase.
SEQUENCE 427 AA; 45824 MW; CE9EEBD29BC641FD CRC64;
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MEDLINE; 97426617.
Blattner F.R., Plunkett
Riley M., Collado-Vides
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                                           FEBS Lett.
                                                                  "Primary structure ribosome.";
                                                                                                      MEDLINE; 80092111.
Wittmann-Liebold B
                                                                                                                                                    STRAIN=K12;
                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                               Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                  Gregor J., Davis N.W.,
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-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                      "The complete genome sequence Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria;
                                         108:69-74(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 01, Created)
(Rel. 21, Last seq
(Rel. 39, Last ann
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                                                                                    of'
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Last annotation update
L23
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                                                                                                           Greuer B
                                                                                    protein
                                                                                                                                                                                                                                                                                    t G. III, Bloch C.A., s J., Glasner J.D., R Kirkpatrick H.A., Go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma
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Pred.
                                                                                         L23
                                                                                                                                                                                                                                           of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subdivision; Enterobacteriaceae;
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                                                                                         from
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No.
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34;
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                                                                                                                                                                                                                                                                                        D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X02613; CAA26462.1; ...
EMBL; U18997; ABS115.1; ...
EMBL; AE000408; AA676343.1; ...
PIR; D23129; R5EC23.
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Morthore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                    "Three vha genes encode proteolipids of Caenorhabditis elegans vacuolar-type ATPase. Gene structures and preferential express: an H-shaped excretory cell and rectal cells."; J. Biol. Chem. 272:24387-24392(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein; rRNA-binding CONFLICT 80 80 MIS SEQUENCE 100 AA; 11199 MW;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPRO01014; ...
PFAM; PF00276; Ribosomal_L23; 1.
PROSITE; PS00050; RIBOSOMAL_L23; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECO2DBASE; 1013.0; 6TH EDITION ECOGENE; EG10883; RPLW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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61 LVVKGK 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Futal M.;
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Last annotation update)
16 KDA PROTEOLIPID SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB
Pred. No. 15;
1; Mismatches
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; 30CD1D77CC7CF9EB CRC64;
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Best Local S
Matches 5
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE
INTEGRAL VO COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RES
FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterson R., Watson A., Wohldman P.; "2.2. Mb of contiguous nu elegans.";
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30
Tobacco mosaic virus (strain tomato/L) (TMV).
                                                                 MOVP_TMVTO P03584;
                                                                                                                                                                                                                                                                      BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
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                                                                                             DIVITO
                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB000918; BAA22596.1; -.
EMBL; Z29095; CAA82355.1; -.
ENER; S40714; S40714.
                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WORMPEP; R10E11.2; CE06290.
INTERPRO; IPRO00245; -.
INTERPRO; IPRO02379; -.
PFAM; PF00137; ATP-synt_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS
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WORMPEP; R10E11.2;
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                                                                                                                                                                           1 MVVKGK
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SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, E C. D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE VO PROTON PORE COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN; WHICH IS PRES AND EAST A HEXAMER THAT FORMS THE PROTON CONDUCTING PORE).

SUBCELLAURAR COATION: INTEGRAL MEMBRANE PROTEIN. VACUOLAR. MISCELLAURADUS: OTHE SUBUNIT BINDS DICYCLOHEXYLCARBODIIMIDE (DCI WHICH INHIBITS THE ATPASE (BY SIMILARITY).
                                                                                                                                                  MVLKGK
                                                                                                                                                                                                     Similarity 83.: 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         family.
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                                                                                                                                                   82
                                                                                                                                                                                                                                                                        AA;
                                                                                STANDARD;
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36
58
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1137
1158
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83.3%;
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DICYCLOHEXYLCARBODIIMIDE (POTENTIAL).
67EDBD2124F12F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                  Score 26; DB
Pred. No. 24;
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POTENTIAL.
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                                                                                                                                                                                                                              Length 161
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RESPONSIBLE
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Matches 5; Conserv
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[14]
SEQUENCE FROM N.A.
MEDLINE; 92113565.
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Seguence FROM N.A.
MEDITUE: 85157522.
Offic T., Acyagi M.,
Okada Y.;
                                                                           INTERPRO:
                                                                                                                          Capuser V.L., Palukaitis P.;
"Nüclectide sequence analysis of the movement genes of resistance with the movement genes of resistance breaking strains of tomato mosaic virus.";

J. Gen. Virol. 73:165-168(1992).

-- 1-4-FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALINEECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X02144; CAA26083.1; -...
PIRE A04182; WMBVT3.
INTERPRO: IPRO01022; -...
PEAN; PF01107; Tobamo MP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thus SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way negligible and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or serious an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                    ON PR-1993 (Rel. 25, Created)
ON APR-1993 (Rel. 25, Last sequence update)
ON APR-1993 (Rel. 25, Last sequence update)
ON APR-1993 (Rel. 25, Last annotation update)
MONIBURE PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
Tomato mosaic virus (strain LIIa).
Violuses; ssrnA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE;
DNA≅binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome and comparison with the common strain J \in \mathbb{B}^{1} ochem. 96:1915-1923(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNAy-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning
protein cistron of
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of the tobacco mosaic virus (tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takamatsu N., Ohno
                        29799;
16APR-1993 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
                                                                                                       JQ1456; WMBVL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR00964; MOVEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83220776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport.
64 AA; 29291 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T., Meshi T., Okada Y.;
and nucleotide sequence of
TMV (tomato strain) genome.
11:3767-3778(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamanashi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.7%;
83.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3B01EB2359AF9C4E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome.
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RESULT MOVE TO DE LO DE 
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local :
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P29800;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).

MOVEMENT PROTEIN (SELT-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calder V.L., Palukaitis P.;

"Nucleotide sequence analysis of the movement genes of resistanc preaking strains of tomato mosaic virus.";

J. Gen. Virol. 73:165-168(1992).

-!- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIAL INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.

PIR; JO1457; WHBUL2.

INTERPRO; ITR001022; -.

INTERPRO; TROBOND_MP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOMVL
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 83299880.
                                                                                                                                                                                                                                                                                                                                  Tobacco mosaic virus (vulgare) (TMV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P03583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding;
SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM MEDLINE; 92113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                             Goelet P., Lomonossoff G.P., Butler P.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOVP_TMV
                                            "Nucleotide sequence of tobacco mosaic virus RNA.";
Proc. Natl. Acad. Sci. U.S.A. 79:5818-5822(1982).
-i- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY
INTECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE
FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION
DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
                                                                                                                                                                                                           Karn J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00964; MOVEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVVKGK 6
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5; Conserv
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92113565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29396 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.7%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽.
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Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4737590A4EB8903B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 AA
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39;
                                                                                                                                                                                                                                .G., Akam M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT RE
Query Match
Best Local S
Matches 5
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Best Local Similarity
Matches 5; Conser
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STAND....

101-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, 
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CHAIN 1 268 27
CHAIN 20 268 27
CHAIN 43 268 29
CHAIN 97 268 19
SEQUENCE 268 AA; 30004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; V01409; CAA24689.1; -
PIR; A04181; WMTM30.
INTERPRO; IPRO01022; -.
                                                                                                                                                                                   DNA-binding; Transport.
SEQUENCE 268 AA; 29961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  PFAM; PF01107; Tobamo_MP; 1.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X68110; -; NOT_ANNOTATED_CDS. PIR; S26359; S26359.
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                                                                                                                                                                                                                                                                     PRINTS; PR00964; MOVEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00964; MOVEMENT.
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FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
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5; Conserv
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27.9 KDA PROTEIN.
25.3 KDA PROTEIN.
19.5 KDA PROTEIN.
19.5 KDA PROTEIN.
W; BE8719A54854FE59 CRC64;
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Pred. No.
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e tobacco
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co mosaic virus
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DNA-binding; Transport.
CHAIN 1 268 27
CHAIN 20 268 27
CHAIN 43 268 25
CHAIN 97 268 19
SEQUENCE 268 AA; 29951 MW;
                                                                                                                                                                                                                                                                   FIBP_ADE15
P36847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.
STRAIN-ISOLATE HXB2956;
MEDLINE; 96074507.
                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
01-NOV-1997 (Rel. 35, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J02412; -; NOT_ANNOTATED_CDS.
EMBL; V01407; CAA24686.1; -.
PIR; A04181; WMTM30.
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J. Biochem. 91:1441-1444(1982).
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                                                                                                Human adenovirus type 1 Viruses; dsDNA viruses,
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                                                                                              Viruses;
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                                                                                                                                                                                            sequence update) annotation update)
                                                                                                RNA stage; Adenoviridae; Mastadenovirus
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27.9 KDA PROTEIN.
25.3 KDA PROTEIN.
19.5 KDA PROTEIN.
19.5 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                         1_HUMAN STANDARD
SBR_HUMAN STANDARD
OB 328;
15-UUL-1999 (Rel. 38, C
15-UUL-1999 (Rel. 38, L
30 MAAY-2000 (Rel. 39, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X72935; CAA51440.1; -.
EMBL; X72936; CAA51441.1; -.
EMBL; X74669; CAA52733.1; -.
PIR; S32663; S32663.
PIR; S37278; S37278.
HSSP; P11818; IKNB.
                                                                                           MEDIVINE: 971/9296.

MEDIVINE: 971/9296.

MEDIVINE: 971/9296.

MEDIVINE: C., Lee C., Waye Chang P.W.G., Tsui S.K.W., Liew C., Lee C., Waye Chang P.W.G., Tsui S.K.W., Liew C., Lee C., Waye Chang P.W.G. and School Change Change and Change Change Control Co
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  This SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                    SEGENBP1 OR SBP.
                                                                                                                                                                                                                                                                                                                                                                                                             SECENIUM-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -# FUNCTION: RECOGNIZES THE CELL RECEPTOR:
BETWEEN THE ADENOVIRUS CAPSID AND THE HOUSE SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO: IPR000931; -.
UNIERPRO: IPR000939; -.
UNIERPRO: IPR000978; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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PRAM; PF00541; adeno_fiber; 1.
PRAMTS; PR00307; ADENOVSFIBRE.
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Virology 206:564-571(1995).
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220 LVVKGK 225
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es 5; Conserv
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                                                                                                                                                                                                                                                           UENCE FROM N.A.
                                              SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SELENIUM-BINDING PROTEIN FAMILY.
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gy 213:313-320(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          .'38, Last sequence update)
. 39, Last annotation update)
PROTEIN 1.
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Pred. No. 52;
1; Mismatches
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                                                                                                                                                                  Lee C., Waye M.M.Y., Fung K.; hromosomal mapping of a novel cDNA
    It is
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  produced through a collaboration
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밁 QΥ

376 LVVKGK

381

1 MVVKGK

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Query Match Best Local

Matches

Similarity 5; Conserv

Conservative

1:

Mismatches

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Indels

0,

Gaps

0

89.7%;

Score 26; Pred. No.

DB 66;

1

Length 472;

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RESULT 14
SBP1_MOUSE
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01-AUG-1990 (Rel. 1
30-MAY-2000 (Rel. 3
SELENIUM-BINDING PR
SELENBP1 OR LPSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selenium.
SEQUENCE
Selenium.
SEQUENCE
                                         EMBL; M32032; AAA40104.1; -. PIR; S27878; S27878.
SWISS-2DPAGE; P17563; MOUSE.
                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                             Carcinogenesis 11:2071-2073(1990).
-!- FUNCTION: NOT KNOWN; BIND SELENIUM.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, KIDNEY AND, 'LESSER EXTENT, LUNG.
-!- SIMILARITY: BELONGS TO THE SELENIUM-BINDING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SBP1_MOUSE P17563;
                                                                                                                                                                                                                                                                                                   implications for selenium'
prevention.";
                                                                                                                                                                                                                                                                                                                                            Bansel M.P., Mukhopadhyay T., Medina D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as
                           MGD; MGI:96825;
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 9102
                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                             "DNA sequencing of a mouse liver protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 LVVKGK
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 472 AA;
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                             SELENBP1.
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. 15, Last sequence update)
. 39, Last annotation update)
PROTEIN 1 (56 KDA SELENIUM-BINDING
 52352 MW;
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83.3%;
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Pred. No.
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Sciurognathi; Muridae; Murinae;
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  D501292C4876033D CRC64;
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There are no restrictions
ng as its content is in
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RESULT 15

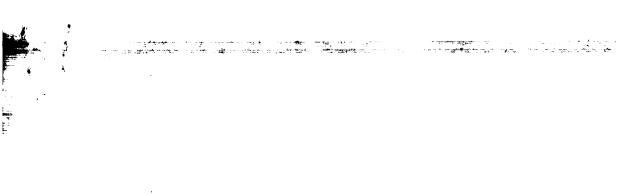
SBP2_MOUSE

SBP2_MOUSE

STANDARD; PRT: 472 AA.

AC 053836;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-1999 (Rel. 38, Last sequence)
DE SELENBP2 OR LPSB2.

OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. (Rel. 11)
RN 121
RN STRAIN-BADG: TISSUE-LIVER:
RN Telacted 56 kDa selenium and acceaminophen-binding proteins in normal related 56 kDa selenium and acceaminophen-binding proteins in normal related 56 kDa selenium binding protein.
RN SEQUENCE OF 175-189; 196-220; 228-242; 290-296; 334-343 AND 399-408.
RN SEQUENCE OF 175-189; 196-220; 228-242; 290-296; 334-343 AND 399-408.
RN SEQUENCE OF 175-189; 196-220; 228-242; 290-296; 334-343 AND 399-408.
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RN SEQUENCE OF 175-189; 196-220; 228-242; 290-296; 334-343 AND 399-408.
RN SEQUENCE OF 185-189; 196-220; 228-242; 290-296; 334-343 AND 399-408.
RN SEQUENCE OF 185-189; 196-220
Search completed: December 14, 2000, 10:14:59 Job time: 224 sec
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                                                                                                                                                                                                                                                                                                                        Query Match 89.7
Best Local Similarity 83.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 175-189; 196-220; 228-242; 290-296; 334-343 AND 399-408 MEDLINE; 92171951
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83.3%;
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       protein search, using sw model
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113...
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sp_virus:*
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PRELIMI.....

O9SZ60;

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O1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
          067338;
067338;
01-AUG-1998
01-AUG-1998
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EU Arabidopsis sequencing project;

EU Arabidopsis sequencing project;

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases

EMBL; AL049638; CAB40936.1; -.

Hypothetical protein.

SEQUENCE 327 AA; 35845 MW; B2BB47DF4A83E635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft
Benorroft I., Newes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL 35.8 KDA PROTEIN.
F16J13.20.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae: Embryophyta; Tracheophyta;
Magnollophyta; eudicotyledons; Rosidae; eurosids II;
Brassicaceae; Arabidopsis.
                                                                                                                                                                                                           1 MVVKGK 6
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275 MVVKGK 28
                                                                                                                                                                                                                                                                                                            y Match 100.0%;
Local Similarity 100.0%;
hes 6; Conservative 0;
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(TrEMBLrel. 07, Last sequence update)
                                                                                      PRELIMINARY;
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074935
Q9XZ53
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067558
Q9YFE1
Q9Y838
Q9Y2V8
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058733
09Y073
09UZG0
09WBI1
09V2A2
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                                                                                                                                                                                                                                                                                                               Score 29; DB
Pred. No. 64;
D; Mismatches
                                                                                        PRT;
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                                                                                      162
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058733 methanococc
099073 lymnaes sta
09uzg0 pyrococcus
09x511 bacillus ce
09x22 pyrococcus
09x511 streptococc
067558 aquifex aeo
09y61 aeropyrum p
09y838 mycosphaere
09v2v8 thermoprote
p93094 cucumis mel
003078 ophioglossu
09zrq0 arabidopsis
018041 caenorhabdi
09xzq6 canine coro
074935 yarrowis li
09xzq6 canine
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Brassicales;
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01-MAY-2000

AY-2000 (TrEMBLrel. DEHYDROGENASE I CHA

I CHAIN J.

Last annotation update)

NADH

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062139
ID 06
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Best Wocal S
Matches 4
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Best Local S
Matches 5
  062139
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059176;
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MWERDPO; IPR001617; -
MWERDPO; IPR001617; -
MYDOTHER TO THE TO T
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Wajikuchi Y., Shizuya H., Kikuchi H.;

Wajikuchi K., Sequence and gene organization of the genome of a hype thermophilic archaebacterium, Pyrococcus horikoshii OT3.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFAM; PF00499; oxidored_q3; 1.
SEQUENCE 162 AA; 17859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000734; AAC07301.1; INTERPRO; IPR001457; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392:353-358(1998)
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Graham D.E., Overbeek R., Snead M.A., Kel
Feldman R.A., Short J.M., Olson G.J., Sw
The complete genome of the hyperthermopl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus horikoshii.
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                                                                                                                     PAIN-OT3;
PDLINE; 98344137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i-AUG-1998 (TrEMBLrel. 07, Created)
i-AUG-1998 (TrEMBLrel. 07, Last sequence update)
i-JUN-2000 (TrEMBLrel. 14, Last annotation update)
pootherical 73.4 KDA PROTEIN PH1507.
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                                                                                                                                                1 MVVKGK 6
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                                                                                                                  MIIKGK
                                                                                                                                                                                                             Similarity 66. 4; Conservative
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5; Conserv
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  PRELIMINARY;
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                                                                                                                                                                                                                                   93.1%;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 28; DB; Pred. No. 52; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asterland T., Young W.G., Lenox A.L., nead M.A., Keller M., Aujay M., Huber Ison G.J., Swanson R.V.; hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                             Score 27; DB Pred. No. 3.7e 2; Mismatches
                                                                                                                                                                                                               2
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ganization of the genome of a hyper-
Pyrococcus horikoshii OT3.";
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  662
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3.7e+02;
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  AA
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nfuku Y.,
Oguchi A.
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1 MVVKGK

Query Match Best Local S Matches 5

Similarity 83.: 5; Conservative

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Best Local S
Matches 4
                                                                                                                                 "Cloning and sequence analysi tobacco mosaic virus.";
Submitted (JUN-1999) to the E EMBL; AF155507; AAD44328.1;
INTERPRO; IPRO01022;
PFAM; PF01107; TOBAMO_MP; 1.
PRINTS; PR00964; MOVEMENT.
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01-AUG-1998 (TrEMBLrel. C
01-AUG-1998 (TrEMBLrel. C
01-MAY-2000 (TrEMBLrel. J
F08A8.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WNG4;
Q9WNG4;
Q1-NOV-1999
01-NOV-1999
01-MAY-2000
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson &
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                    26.8
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INTERPRO; IPRO02655; -.
PFAM; PF01756; ACOX; 1.
SEQUENCE 662 AA; 74770
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                                                                                                                                                                                                                                                                                               Sheng Q.B.,
                                                                                                                                                                                                                                                                                                                                                                                       Tobacco mosaic virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 93.1%;
Similarity 66.7%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                               Gong Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                 26802
                         89.7%;
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13,
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13,
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                                                                                                               MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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Last sequence up
Score 26; DB 12;
Pred. No. 2.3e+02;
1; Mismatches 0;
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3.9e+02;
0;
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                                            Length 242
                                                                                                                 CRC64
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"Mutation in the tobacco mosaic virus 30-KD prote
Za resistance in tomato.";
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ dat
EMBL; D17458; BAA04268.1; -.
INTERPRO; IRRO01072; -.
PFAM; PF01107; TObamo_MP; 1.
PRINTS; PR01964; MOVEMENT.
SEQUENCE 264 AA; 29362 MW; 36B7EA334F1939D8 (
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01-MAY-1999 (
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Q83481;
                                                         Zhou X., Xue C., Q1 Y., L1 D.;
"Isolation and nucleotide sequence of the 30k cistron of a Chinese isolate of tomato mosaic Submitted (CCT-1998) to the EMBL/GenBank/DDBJ EMBL; AJ013845; CAB36999.1; --
EMBL; AJ011934; CAA09878.1; --
INTERPRO; IPR001022; --
PFAM; PF01107; Tobamo_MP; 1.
PRINTS; PR00964; MOVEMENT.
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Tobacco mosaic virus.
Viruses; ssRNA positive-strand viruses,
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"Complete nucleotide sequence and synthesis of infi-
transcripts from a full length cDNA clone of a rak-
tobacco mosaic virus.";
Arch. Virol. 141:885-900(1996).
EMBL; D63809; BAA09878:1; -.
INTERPRO; IPRO01022; -.
PFAM; PF01107; Tobamo_MP; 1.
PRINTS; PR00964; MOVEMENT.
SEQUENCE 268 AA; 29849 MW; 2E843BE774DF312F CR0
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091275;
01-NOV-1998
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Q98746;
Q1-FEB-1997
Q1-FEB-1997
Q1-MAY-2000
                                                      "Complete nucleotide sequence and genome organ mosaic virus isolated from Vicia faba."; Submitted (OCT-1998) to the EMBL/GenBanK/DDBJ EMBL; AJ006991; CAA07412.1; -. EMBL; AJ011933; CAA09876.1; -. INTERPRO; IPRO01022; -. INTERPRO; TPRO01022; -. PFAM; PF01107; Tobamo_MP; 1.
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MEDLINE; 96265
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Xue C., Zhou X., Chen Q., Q1 Y.,
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"Cloning and sequence analysis of Submitted (JUL-1999) to the EMBI EMBL; AF165190; AAD47819.1; -...

"EMBERRA"; IFR001022; -...

"ERINTS; PR00107; Tobamo_MP; 1.

"FRINTS; PR00964; MOVEMENT.

"FROUENCE 268 AA; 29942 MW; 1
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Brassicaceae; Arabidopsis.
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II;
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SEQUENCE FROM N.A.

PETERS S.A., Van Staveren M., Dirkse W., Stiekema W., Bancroft Medes H.W., Mayer K.F.X., Schueller C., Bevan M.; Medes H.W., Mayer K.F.X., Schueller C., Bevan M.; Summitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AL031018; CAA19805.1; •.

HMBOChetical protein.

SEQUENCE 333 AA; 36350 MW; A700BA7FB93F9EDB CRC64;
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                                                                                                                                      89.7%;
83.3%;
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Pred.
1; Mis
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Last sequence up
Last annotation
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1; Mismatches 0;
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                                                                                                                      Mismatches
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                                                                                                                                      26; DB 10;
No. 3.2e+02;
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2.5e+02;
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Brassicales;
                                                                                                                    0;
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032178
ID 032178
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Matches 5
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Best Local :
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SEQUENCE 502 AF
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088537;
01-NOV-1998
01-NOV-1998
01-JUN-2000
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01-MAY-2000
01-MAY-2000
01-MAY-2000
 032178
                                                                                                                                                                                                                                                                                            Rooker M.M., Sherburne C., Lav
"Characterization of the Tra2
Plasmid 41:226-239(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gao J.-L., Chen H., Filie J.D., "Differential expansion of the N in human and mouse."; Genomics 51:270-276(1998).

EMBL: AF071181; AAC34586.1; -.
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Mus musculus (Mouse).

Mus musculus (Mouse).

Chordata;

Charvota; Metazoa; Chordata;

Rodentia;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 99296679.
                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi
Plasmid R27
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PFAM; PF00001; 7tm_1; 1.

PRINTS; PR00023; GPCRIDOPSN.

PRINTS; PR00526; FMETLEUPHER.

PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

SEQUENCE 343 AA; 38111 MW; 0F726BF195CBFB29
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
N-FORMYLPEPTIDE RECEPTOR-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
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                                                                                    242 LVVKGK
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nes 5; Conserv
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5; Conser
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83
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Pred. No. 5e+02;
1; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                              wley T.D.,
region of
 PRT;
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3.3e+02;
hes 0;
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the IncHI1 plasmid
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RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Takagi T., Takahashi H., Takemaru K.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassanotti A.,
RA Vlari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamame K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamame K., Yasumoto K., Yata K.,
RA Woshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 5
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Submitted (NOV-1997) to the
EMBL: 299120; CAB15273.1;
INTERPRO: IPRO01205;
INTERPRO: IPRO01753;
INTERPRO: IPRO02135;
Q9UYR5;
Q9UYR5;
01-MAY-2000
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00378; ECH; 1.
PFAM; PF00725; 3HCDH;
SEQUENCE 815 AA; 90
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Kunst F., Ogasawai
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Bacteria; Firmicutes;
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90148 MW;
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83.3%;
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us group; Bacillus.
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., Bessieres P., Bolotin A., Borche
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the EMBL/GenBank/DDBJ
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1; Mismatches
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8.3e+02;
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Submitted (JUL-1999) to the
EMBL; AJ248287: CAB50347.1;
INTERPRO: IPRO02145: -.
PFAM: PF01402: HTH.4; 1.
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Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ORSAY;
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                                                                                                                                                                                                                                                                         1 MVVKGK 6
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| IVVKGK 106
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5; Conservative
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138 AA; 1
                                    December 14,
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1; Mismatches
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